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(54) Title: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

(57) Abstract: Nucleic acids encoding mammalian, e.g., primate, receptors, purified receptor proteins and fragments thereof. Antibodies, both polyclonal and monoclonal, are also provided. Methods of using the compositions for both diagnostic and therapeutic utilities are described.

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MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

FIELD OF THE INVENTION

The present invention relates to compositions and methods for affecting mammalian physiology, including immune system function. In particular, it provides methods to regulate development and/or the immune system. Diagnostic and therapeutic uses of these materials are also disclosed.

BACKGROUND OF THE INVENTION

Recombinant DNA technology refers generally to techniques of integrating genetic information from a donor source into vectors for subsequent processing, such as through introduction into a host, whereby the transferred genetic information is copied and/or expressed in the new environment. Commonly, the genetic information exists in the form of complementary DNA (cDNA) derived from messenger RNA (mRNA) coding for a desired protein product. The carrier is frequently a plasmid having the capacity to incorporate cDNA for later replication in a host and, in some cases, actually to control expression of the cDNA and thereby direct synthesis of the encoded product in the host. See, e.g., Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual, (2d ed.) vols. 1-3, CSH Press, NY.

For some time, it has been known that the mammalian immune response is based on a series of complex cellular interactions, called the "immune network". Recent research has provided new insights into the inner workings of this network. While it remains clear that much of the immune response does, in fact, revolve around the network-like interactions of lymphocytes, macrophages, granulocytes, and other cells, immunologists now generally hold the opinion that soluble proteins, known as lymphokines, cytokines, or monokines, play critical roles in controlling these cellular interactions. Thus, there is considerable interest in the isolation, characterization, and mechanisms of action of cell modulatory factors, an understanding of which will lead to significant advancements in the diagnosis and therapy of numerous medical abnormalities, e.g., immune system disorders.

The immune system of vertebrates consists of a number of organs and several different cell types. Two major cell types include the myeloid and lymphoid lineages. Among the lymphoid cell lineage are B cells, which were originally characterized as differentiating in fetal liver or adult bone marrow, and T cells, which were originally characterized as differentiating in the thymus. See, e.g., Paul (ed. 1998) Fundamental Immunology (4th ed.) Raven Press, New York; and Thomson (ed. 1994) The Cytokine Handbook 2d ed., Academic Press, San Diego. Lymphokines apparently mediate cellular activities in a variety of ways. They have been shown to support the proliferation, growth, and/or differentiation of cells, e.g., pluripotential hematopoietic stem cells, into vast numbers of progenitors comprising diverse cellular lineages which make up a complex immune system. Proper and balanced interactions between the cellular components are necessary for a healthy immune response. The different cellular lineages often respond in a different manner when lymphokines are administered in conjunction with other agents.

Cell lineages especially important to the immune response include two classes of lymphocytes: B-cells, which can produce and secrete immunoglobulins (proteins with the capability of recognizing and binding to foreign matter to effect its removal), and T-cells of various subsets that secrete lymphokines and induce or suppress the B-cells and various other cells (including other T-cells) making up the immune network. These lymphocytes interact with many other cell types.

Research to better understand and treat various immune disorders has been hampered by the general inability to maintain cells of the immune system in vitro. Immunologists have discovered that culturing many of these cells can be accomplished through the use of T-cell and other cell supernatants, which contain various growth factors, including many of the lymphokines.

Various growth and regulatory factors exist which modulate morphogenetic development. And many receptors for cytokines are also known. Often there are at least two critical subunits in the functional receptor. See, e.g., Gonda and D'Andrea (1997) Blood 89:355-369; Presky, et al. (1996) Proc. Nat'l Acad. Sci. USA 93:14002-14007; Drachman and Kaushansky (1995) Curr. Opin. Hematol. 2:22-28; Theze (1994) Eur. Cytokine Netw. 5:353-368; and Lemmon and Schlessinger (1994) Trends Biochem. Sci. 19:459-463.

From the foregoing, it is evident that the discovery and development of new soluble proteins and their receptors, including ones similar to lymphokines, should contribute to new therapies for a wide range of degenerative or abnormal conditions which directly or indirectly involve development, differentiation, or function, e.g., of the

immune system and/or hematopoietic cells. In particular, the discovery and understanding of novel receptors for lymphokine-like molecules which enhance or potentiate the beneficial activities of other lymphokines would be highly advantageous. However, the lack of understanding of how the immune system is regulated or differentiates has blocked the ability to advantageously modulate the normal defensive mechanisms to biological challenges. Medical conditions characterized by abnormal or inappropriate regulation of the development or physiology of relevant cells thus remain unmanageable. The discovery and characterization of specific cytokines and their receptors will contribute to the development of therapies for a broad range of degenerative or other conditions which affect the immune system, hematopoietic cells, as well as other cell types. The present invention provides new receptors for ligands exhibiting similarity to cytokine like compositions and related compounds, and methods for their use.

SUMMARY OF THE INVENTION

The present invention is directed to novel receptors related to cytokine receptors, e.g., primate, cytokine receptor like molecular structures, designated DNAX Cytokine Receptor Subunits (DCRS), and their biological activities. In particular, it provides description of various subunits, designated DCRS6, DCRS7, DCRS8, DCRS9, and DCRS10. Primate, e.g, human, and rodent, e.g., mouse, embodiments of the various subunits are provided. It includes nucleic acids coding for the polypeptides themselves and methods for their production and use. The nucleic acids of the invention are characterized, in part, by their homology to cloned complementary DNA (cDNA) sequences enclosed herein.

The present invention provides a composition of matter selected from: a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 2, 5, 8, 11, 23, or 26; a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 14; a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 14; a natural sequence DCRS8 comprising mature SEQ ID NO: 14; a fusion polypeptide comprising DCRS8 sequence; a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 17 or 20; a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 17 or 20; a natural

sequence DCRS9 comprising mature SEQ ID NO: 17 or 20; or a fusion polypeptide comprising DCRS9 sequence. Preferably, wherein the distinct nonoverlapping segments of identity include: one of at least eight amino acids; one of at least four amino acids and a second of at least five amino acids; at least three segments of at least four, five, and six amino acids, or one of at least twelve amino acids. In other embodiments, the: polypeptide: comprises a mature sequence of Tables 1, 2, 3, 4, or 5; is an unglycosylated form of DCRS8 or DCRS9; is from a primate, such as a human; comprises at least seventeen amino acids of SEQ ID NO: 14 or 17; exhibits at least four nonoverlapping segments of at least seven amino acids of SEQ ID NO: 14 or 17; is a natural allelic variant of DCRS8 or DCRS9; has a length at least about 30 amino acids; exhibits at least two non-overlapping epitopes which are specific for a primate DCRS8 or DCRS9; is glycosylated; has a molecular weight of at least 30 kD with natural glycosylation; is a synthetic polypeptide; is attached to a solid substrate; is conjugated to another chemical moiety; is a 5-fold or less substitution from natural sequence; or is a deletion or insertion variant from a natural sequence.

The invention further embraces a composition comprising: a substantially pure DCRS8 or DCRS9 and another cytokine receptor family member; a sterile DCRS8 or DCRS9 polypeptide; the DCRS8 or DCRS9 polypeptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration. Additional embodiments include a polypeptide comprising: mature protein sequence of Tables 1, 2, 3, 4, or 5; a detection or purification tag, including a FLAG, His6, or Ig sequence; or sequence of another cytokine receptor protein. Kit embodiments include ones comprising a described polypeptide, and: a compartment comprising the protein or polypeptide; or instructions for use or disposal of reagents in the kit.

Binding compositions are provided, e.g., comprising an antigen binding site from an antibody, which specifically binds to a natural DCRS8 or DCRS9 polypeptide, wherein: the binding compound is in a container; the DCRS8 or DCRS9 polypeptide is from a human; the binding compound is an Fv, Fab, or Fab2 fragment; the binding compound is conjugated to another chemical moiety; or the antibody: is raised against a peptide sequence of a mature polypeptide of Table 3 or 4; is raised against a mature DCRS8 or DCRS9; is raised to a purified human DCRS8 or DCRS9; is immunoselected; is a polyclonal antibody; binds to a denatured DCRS8 or DCRS9; exhibits a Kd to antigen of at least 30 μM; is attached to a solid substrate, including a bead or plastic membrane; is in a sterile composition; or is detectably labeled, including a radioactive or fluorescent label. Kits include ones comprising such a binding compound, and: a compartment

comprising the binding compound; or instructions for use or disposal of reagents in the kit.

The invention also provides methods of producing an antigen:antibody complex, comprising contacting under appropriate conditions a primate DCRS8 or DCRS9 polypeptide with a described antibody, thereby allowing the complex to form. Preferred methods include ones wherein: the complex is purified from other cytokine receptors; the complex is purified from other antibody; the contacting is with a sample comprising an interferon; the contacting allows quantitative detection of the antigen; the contacting is with a sample comprising the antibody; or the contacting allows quantitative detection of the antibody. Further compositions include those comprising: a sterile binding compound, as described, or the binding compound and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration.

Nucleic acid compositions include an isolated or recombinant nucleic acid encoding a desribed polypeptide wherein the: DCRS8 or DCRS9 is from a human; or the nucleic acid: encodes an antigenic peptide sequence of Table 3 or 4; encodes a plurality of antigenic peptide sequences of Table 3 or 4; exhibits identity over at least thirteen nucleotides to a natural cDNA encoding the segment; is an expression vector; further comprises an origin of replication; is from a natural source; comprises a detectable label; comprises synthetic nucleotide sequence; is less than 6 kb, preferably less than 3 kb; is from a primate; comprises a natural full length coding sequence; is a hybridization probe for a gene encoding the DCRS8 or DCRS9; or is a PCR primer, PCR product, or mutagenesis primer. Also provided are a cell or tissue comprising such a recombinant nucleic acid, e.g., where the cell is: a prokaryotic cell; a eukaryotic cell; a bacterial cell; a yeast cell; an insect cell; a mammalian cell; a mouse cell; a primate cell; or a human cell.

Kit embodiments include those comprising a described nucleic acid and: a compartment comprising the nucleic acid; a compartment further comprising a primate DCRS8 or DCRS9 polypeptide; or instructions for use or disposal of reagents in the kit.

Other nucleic acids provided include ones which: hybridize under wash conditions of 30 minutes at 30° C and less than 2M salt to the coding portion of SEQ ID NO: 13 or 16; or exhibit identity over a stretch of at least about 30 nucleotides to a primate DCRS8 or DCRS9. Preferably, such will be nucleic acids where: the wash conditions are: at 45° C and/or 500 mM salt; at 55° C and/or 150 mM salt; or the stretch is at least 55 or 75 nucleotides.

Also provided are methods of modulating physiology or development of a cell or tissue culture cells comprising contacting the cell with an agonist or antagonist of a

mammalian DCRS8 or DCRS9. Preferably, the cell is transformed with a nucleic acid encoding the DCRS8 or DCRS9 and another cytokine receptor subunit.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

OUTLINE

I. General
II. Activities
III. Nucleic acids
  A. encoding fragments, sequence, probes
  B. mutations, chimeras, fusions
  C. making nucleic acids
  D. vectors, cells comprising
IV. Proteins, Peptides
  A. fragments, sequence, immunogens, antigens
  B. muteins
  C. agonists/antagonists, functional equivalents
  D. making proteins
V. Making nucleic acids, proteins
  A. synthetic
  B. recombinant
  C. natural sources
VI. Antibodies
  A. polyclonals
  B. monoclonal
  C. fragments; Kd
  D. anti-idiotypic antibodies
  E. hybridoma cell lines
VII. Kits and Methods to quantify DCRSs
  A. ELISA
  B. assay mRNA encoding
  C. qualitative/quantitative
  D. kits
VIII. Therapeutic compositions, methods
  A. combination compositions
  B. unit dose
  C. administration
IX. Screening
X. Ligands

I. General

The present invention provides the amino acid sequence and DNA sequence of mammalian, herein primate, cytokine receptor-like subunit molecules, these designated DNAX Cytokine Receptor Subunits 6 (DCRS6), 7 (DCRS7), 8 (DCRS8), 9 (DCRS9), and 10 (DCRS10) having particular defined properties, both structural and biological.

Various cDNAs encoding these molecules were obtained from primate, e.g., human, and/or rodent, e.g., mouse, cDNA sequence libraries. Other primate or other mammalian counterparts would also be desired.

Some of the standard methods applicable are described or referenced, e.g., in Maniatis, et al. (1982) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor Press; Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual, (2d ed.), vols. 1-3, CSH Press, NY; Ausubel, et al., Biology, Greene Publishing Associates, Brooklyn, NY; or Ausubel, et al. (1987 and periodic supplements) Current Protocols in Molecular Biology, Greene/Wiley, New York; each of which is incorporated herein by reference.

Nucleotide (SEQ ID NO: 1) and corresponding amino acid sequence (SEQ ID NO: 2) of a primate, e.g., human, DCRS6 coding segment is shown in Table 1 along with reverse translation (SEQ ID NO: 3). Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 4-6.

Similarly, nucleotide (SEQ ID NO: 7) and corresponding amino acid sequence (SEQ ID NO: 8) of a primate, e.g., human, DCRS7 coding segment is shown in Table 2 along with reverse translation (SEQ ID NO: 9). Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 10-12. Nucleotide (SEQ ID NO: 13) and corresponding amino acid sequence (SEQ ID NO: 14) of a primate, e.g., human, DCRS8 coding segment is shown in Table 3 along with reverse translation (SEQ ID NO: 15).

Nucleotide (SEQ ID NO: 16) and corresponding amino acid sequence (SEQ ID NO: 17) of a primate, e.g., human, DCRS9 coding segment is shown in Table 4 along with reverse translation (SEQ ID NO: 18). Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 19-21. Nucleotide (SEQ ID NO: 22) and corresponding amino acid sequence (SEQ ID NO: 23) of a primate, e.g., human, DCRS10 coding segment is shown in Table 5 along with reverse translation (SEQ ID NO: 24). Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 26-27.

Table 1: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiments (DCRS6). Primate, e.g., human, embodiment (see SEQ ID NO: 1 and 2). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

```
gcg atg tcg ctc gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc   48
    Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala
                    -10                     -5              -1   1

gta ccc cga gag ccg acc gtt caa tgt ggc tct gaa act ggg cca tct   96
Val Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser
            5                   10                  15
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cca gag tgg atg cta caa cat gat cta atc ccg gga gac ttg agg gac   144
Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp
         20                  25                  30

ctc cga gta gaa cct gtt aca act agt gtt gca aca ggg gac tat tca   192
Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser
     35                  40                  45

att ttg atg aat gta agc tgg gta ctc cgg gca gat gcc agc atc cgc   240
Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg
 50                  55                  60                  65

ttg ttg aag gcc acc aag att tgt gtg acg ggc aaa agc aac ttc cag   288
Leu Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln
                 70                  75                  80

tcc tac agc tgt gtg agg tgc aat tac aca gag gcc ttc cag act cag   336
Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln
             85                  90                  95

acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tat atc ggc ttc cct   384
Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro
        100                 105                 110

gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat att cct aat   432
Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn
    115                 120                 125

gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat ttc acc tca   480
Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser
130                 135                 140                 145

cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag tgt gtc aag   528
Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys
                150                 155                 160

gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag aag aat gag   576
Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu
            165                 170                 175

gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga aac aga tac   624
Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr
        180                 185                 190

atg gct ctt atc caa cac agc act atc atc ggg ttt tct cag gtg ttt   672
Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe
    195                 200                 205

gag cca cac cag aag aaa caa acg cga gct tca gtg gtg att cca gtg   720
Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val
210                 215                 220                 225

act ggg gat agt gaa ggt gct acg gtg cag ctg act cca tat ttt cct   768
Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro
                230                 235                 240
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act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc   816
Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys
            245                 250                 255

cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa agc aag ccg   864
Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro
        260                 265                 270

gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg   912
Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp
    275                 280                 285

gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa agg atc aag   960
Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys
290                 295                 300                 305

aag act tcc ttt tct acc acc aca cta ctg ccc ccc att aag gtt ctt   1008
Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu
                310                 315                 320

gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att tgt tac ttc   1056
Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe
            325                 330                 335

act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc ctt gaa aag   1104
Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys
        340                 345                 350

tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc   1152
Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala
    355                 360                 365

act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt tcc aat gac   1200
Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp
370                 375                 380                 385

gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc   1248
Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro
                390                 395                 400

agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc   1296
Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys
            405                 410                 415

agt gat cta aga agc cag att cat ctg cac aaa tac gtg gtg gtc tac   1344
Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr
        420                 425                 430

ttt aga gag att gat aca aaa gac gat tac aat gct ctc agt gtc tgc   1392
Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys
    435                 440                 445

ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt   1440
Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu
450                 455                 460                 465
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```
ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc   1488
Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys
                470                 475                 480

cac gat ggc tgc tgc tcc ttg tagcccaccc atgagaagca agagacctta     1539
His Asp Gly Cys Cys Ser Leu
            485

aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgatcctga agcttactat 1599

gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaatt ttcaaatatt 1659

gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt 1719

tatacataga aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca 1779

ataaagcatc ttcagcc                                                1796
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MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTSVATGDYSILMNVSWVL
RADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPNA
NMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQHSTI
IGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVPFPLDNNKSKPG
GWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFLQNHCR
SEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCS
DLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL.

Reverse translation of primate, e.g., human, DCRS6 (SEQ ID NO: 3):

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atgwsnytng tnytnytnws nytngcngcn ytntgymgnw sngcngtncc nmgngarccn 60

acngtncart gyggnwsnga racnggnccn wsnccngart ggatgytnca rcaygayytn 120

athccnggng ayytnmgnga yytnmgngtn garccngtna cnacnwsngt ngcnacnggn 180

gaytaywsna thytnatgaa ygtnwsntgg gtnytnmgng cngaygcnws nathmgnytn 240

ytnaargcna cnaarathtg ygtnacnggn aarwsnaayt tycarwsnta ywsntgygtn 300

mgntgyaayt ayacngargc nttycaracn caracnmgnc cnwsnggngg naartggacn 360

ttywsntaya thggnttycc ngtngarytn aayacngtnt ayttyathgg ngcncayaay 420

athccnaayg cnaayatgaa ygargayggn ccnwsnatgw sngtnaaytt yacnwsnccn 480

ggntgyytng aycayathat gaartayaar aaraartgyg tnaargcngg nwsnytntgg 540

gayccnaaya thacngcntg yaaraaraay gargaracng tngargtnaa yttyacnacn 600

acnccnytng gnaaymgnta yatggcnytn athcarcayw snacnathat hggnttywsn 660

cargtnttyg arccncayca raaraarcar acnmgngcnw sngtngtnat hccngtnacn 720

ggngaywsng arggngcnac ngtncarytn acnccntayt tyccnacntg yggnwsngay 780

tgyathmgnc ayaarggnac ngtngtnytn tgyccncara cnggngtncc nttyccnytn 840

gayaayaaya arwsnaarcc nggnggntgg ytnccnytny tnytnytnws nytnytngtn 900
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gcnacntggg tnytngtngc nggnathtay ytnatgtggm gncaygarmg nathaaraar 960
acnwsnttyw snacnacnac nytnytnccn ccnathaarg tnytngtngt ntayccnwsn 1020
garathtgyt tycaycayac nathtgytay ttyacngart tyytncaraa ycaytgymgn 1080
wsngargtna thytngaraa rtggcaraar aaraarathg cngaratggg nccngtncar 1140
tggytngcna cncaraaraa rgcngcngay aargtngtnt tyytnytnws naaygaygtn 1200
aaywsngtnt gygayggnac ntgyggnaar wsngarggnw snccnwsnga raaywsncar 1260
gayytnttyc cnytngcntt yaayytntty tgywsngayy tnmgnwsnca rathcayytn 1320
cayaartayg tngtngtnta yttymgngar athgayacna argaygayta yaaygcnytn 1380
wsngtntgyc cnaartayca yytnatgaar gaygcnacng cnttytgygc ngarytnytn 1440
caygtnaarc arcargtnws ngcnggnaar mgnwsncarg cntgycayga yggntgytgy 1500
wsnytn                                                            1506
```

Rodent, e.g., mouse embodiment (see SEQ ID NO: 4 and 5).

```
gat ttc agc agc cag acg cat ctg cac aaa tac ctg gag gtc tat ctt    48
Asp Phe Ser Ser Gln Thr His Leu His Lys Tyr Leu Glu Val Tyr Leu
 1               5                  10                  15

ggg gga gca gac ctc aaa ggc gac tat aat gcc ctg agt gtc tgc ccc    96
Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
            20                  25                  30

caa tat cat ctc atg aag gac gcc aca gct ttc cac aca gaa ctt ctc    144
Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
        35                  40                  45

aag gct acg cag agc atg tca gtg aag aaa cgc tca caa gcc tgc cat    192
Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
    50                  55                  60

gat agc tgt tca ccc ttg tagtccaccc gggggaatag agactctgaa           240
Asp Ser Cys Ser Pro Leu
 65                 70

gccttcctac tctcccttcc agtgacaaat gctgtgtgac gactctgaaa tgtgtgggag 300
aggctgtgtg gaggtagtgc tatgtacaaa cttgctttaa aactggagtt tgcaaagtca 360
acctgagcat acacgcctga ggctagtcat tggctggatt tatgaagaca acacagttac 420
agacaataat gagtgggacc tacatttggg atatacccaa agctgggtaa tgattatcac 480
tgagaaccac gcactctggc catgaggtaa tacggcactt ccctgtcagg ctgtctgtca 540
ggttgggtct gtcttgcact gcccatgctc tatgctgcac gtagaccgtt ttgtaacatt 600
ttaatctgtt aatgaataat ccgtttggga ggctctc                          637
```

DFSSQTHLHKYLEVYLGGADLKGDYNALSVCPQYHLMKDATAFHTELLKATQSMSVKKRSQACHDSCSPL.

Reverse translation of rodent, e.g., mouse, DCRS6 (SEQ ID NO: 6):

```
gayttywsnw sncaracnca yytncayaar tayytngarg tntayytngg nggngcngay 60

ytnaarggng aytayaaygc nytnwsngtn tgyccncart aycayytnat gaargaygcn 120

acngcnttyc ayacngaryt nytnaargcn acncarwsna tgwsngtnaa raarmgnwsn 180

cargcntgyc aygaywsntg ywsnccnytn                                 210
```

Table 2: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiments (DCRS7). Primate, e.g., human, embodiment (see SEQ ID NO: 7 and 8). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

```
gagtcaggac tcccaggaca gagagtgcac aaactaccca gcacagcccc ctccgccccc 60

tctggaggct gaagagggat tccagcccct gccacccaca gacacgggct gactggggtg 120

tctgcccccc ttgggggcan ccacagggcc tcaggcctgg gtgccacctg gcactagaag 180

atg cct gtg ccc tgg ttc ttg ctg tcc ttg gca ctg ggc cga agc cag    228
Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
-20                 -15                 -10                  -5

tgg atc ctt tct ctg gag agg ctt gtg ggg cct cag gac gct acc cac    276
Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
             -1   1               5                  10

tgc tct ccg ggc ctc tcc tgc cgc ctc tgg gac agt gac ata ctc tgc    324
Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
        15                  20                  25

ctg cct ggg gac atc gtg cct gct ccg ggc ccc gtg ctg gcg cct acg    372
Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
    30                  35                  40

cac ctg cag aca gag ctg gtg ctg agg tgc cag aag gag acc gac tgt    420
His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
45                  50                  55                  60

gac ctc tgt ctg cgt gtg gct gtc cac ttg gcc gtg cat ggg cac tgg    468
Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
                65                  70                  75

gaa gag cct gaa gat gag gaa aag ttt gga gga gca gct gac tta ggg    516
Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
            80                  85                  90

gtg gag gag cct agg aat gcc tct ctc cag gcc caa gtc gtg ctc tcc    564
Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
        95                 100                 105
```

```
ttc cag gcc tac cct act gcc cgc tgc gtc ctg ctg gag gtg caa gtg    612
Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
    110                 115                 120

cct gct gcc ctt gtg cag ttt ggt cag tct gtg ggc tct gtg gta tat    660
Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
125                 130                 135                 140

gac tgc ttc gag gct gcc cta ggg agt gag gta cga atc tgg tcc tat    708
Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
                145                 150                 155

act cag ccc agg tac gag aag gaa ctc aac cac aca cag cag ctg cct    756
Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
            160                 165                 170

gac tgc agg ggg ctc gaa gtc tgg aac agc atc ccg agc tgc tgg gcc    804
Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala
        175                 180                 185

ctg ccc tgg ctc aac gtg tca gca gat ggt gac aac gtg cat ctg gtt    852
Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val
    190                 195                 200

ctg aat gtc tct gag gag cag cac ttc ggc ctc tcc ctg tac tgg aat    900
Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn
205                 210                 215                 220

cag gtc cag ggc ccc cca aaa ccc cgg tgg cac aaa aac ctg act gga    948
Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly
                225                 230                 235

ccg cag atc att acc ttg aac cac aca gac ctg gtt ccc tgc ctc tgt    996
Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys
            240                 245                 250

att cag gtg tgg cct ctg gaa cct gac tcc gtt agg acg aac atc tgc    1044
Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys
        255                 260                 265

ccc ttc agg gag gac ccc cgc gca cac cag aac ctc tgg caa gcc gcc    1092
Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala
    270                 275                 280

cga ctg cga ctg ctg acc ctg cag agc tgg ctg ctg gac gca ccg tgc    1140
Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys
285                 290                 295                 300

tcg ctg ccc gca gaa gcg gca ctg tgc tgg cgg gct ccg ggt ggg gac    1188
Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp
                305                 310                 315

ccc tgc cag cca ctg gtc cca ccg ctt tcc tgg gag aat gtc act gtg    1236
Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr Val
            320                 325                 330

gac gtg aac agc tcg gag aag ctg cag ctg cag gag tgc ttg tgg gct    1284
Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala
        335                 340                 345
```

```
gac tcc ctg ggg cct ctc aaa gac gat gtg cta ctg ttg gag aca cga    1332
Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg
    350                 355                 360

ggc ccc cag gac aac aga tcc ctc tgt gcc ttg gaa ccc agt ggc tgt    1380
Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys
365                 370                 375                 380

act tca cta ccc agc aaa gcc tcc acg agg gca gct cgc ctt gga gag    1428
Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu
                385                 390                 395

tac tta cta caa gac ctg cag tca ggc cag tgt ctg cag cta tgg gac    1476
Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp
            400                 405                 410

gat gac ttg gga gcg cta tgg gcc tgc ccc atg gac aaa tac atc cac    1524
Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His
        415                 420                 425

aag cgc tgg gcc ctc gtg tgg ctg gcc tgc cta ctc ttt gcc gct gcg    1572
Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala
    430                 435                 440

ctt tcc ctc atc ctc ctt ctc aaa aag gat cac gcg aaa ggg tgg ctg    1620
Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu
445                 450                 455                 460

agg ctc ttg aaa cag gac gtc cgc tcg ggg gcg gcc gcc agg ggc cgc    1668
Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg Gly Arg
                465                 470                 475

gcg gct ctg ctc ctc tac tca gcc gat gac tcg ggt ttc gag cgc ctg    1716
Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu
            480                 485                 490

gtg ggc gcc ctg gcg tcg gcc ctg tgc cag ctg ccg ctg cgc gtg gcc    1764
Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala
        495                 500                 505

gta gac ctg tgg agc cgt cgt gaa ctg agc gcg cag ggg ccc gtg gct    1812
Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala
    510                 515                 520

tgg ttt cac gcg cag cgg cgc cag acc ctg cag gag ggc ggc gtg gtg    1860
Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val
525                 530                 535                 540

gtc ttg ctc ttc tct ccc ggt gcg gtg gcg ctg tgc agc gag tgg cta    1908
Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu
                545                 550                 555

cag gat ggg gtg tcc ggg ccc ggg gcg cac ggc ccg cac gac gcc ttc    1956
Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe
            560                 565                 570
```

```
cgc gcc tcg ctc agc tgc gtg ctg ccc gac ttc ttg cag ggc cgg gcg    2004
Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala
    575                 580                 585

ccc ggc agc tac gtg ggg gcc tgc ttc gac agg ctg ctc cac ccg gac    2052
Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp
    590                 595                 600

gcc gta ccc gcc ctt ttc cgc acc gtg ccc gtc ttc aca ctg ccc tcc    2100
Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser
605                 610                 615                 620

caa ctg cca gac ttc ctg ggg gcc ctg cag cag cct cgc gcc ccg cgt    2148
Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg
                625                 630                 635

tcc ggg cgg ctc caa gag aga gcg gag caa gtg tcc cgg gcc ctt cag    2196
Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
            640                 645                 650

cca gcc ctg gat agc tac ttc cat ccc ccg ggg acn tcc gcg ccg gga    2244
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly
        655                 660                 665

cgc ggg gtg gga cca ggg gcg gga cct ggg gcg ggg gac ggg act        2289
Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr
    670                 675                 680

taaataaagg cagacgctg                                               2308
```

```
MPVPWFLLSLALGRSQWILSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPVLAPTHLQTELVL
RCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADLGVEEPRNASLQAQVVLSFQAYPTARCVLLEVQV
PAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPDCRGLEVWNSIPSCWALPWLNVSA
DGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNIC
PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDVNSSEKL
QLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYLLQDLQSGQCLQLWD
DDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKGWLRLLKQDVRSGAAARGRAALLLYSA
DDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWL
QDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGA
LQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTSAPGRGVGPGAGPGAGDGT.
```

Reverse translation of primate, e.g., human, DCRS7 (SEQ ID NO: 9):

```
atgccngtnc cntggttyyt nytnwsnytn gcnytnggnm gnwsncartg gathytnwsn 60
ytngarmgny tngtnggncc ncargaygcn acncaytgyw snccnggnyt nwsntgymgn 120
ytntgggayw sngayathyt ntgyytnccn ggngayathg tnccngcncc nggnccngtn 180
ytngcnccna cncayytnca racngarytn gtnytnmgnt gycaraarga racngaytgy 240
gayytntgyy tnmgngtngc ngtncayytn gcngtncayg gncaytggga rgarccngar 300
gaygargara arttyggngg ngcngcngay ytnggngtng argarccnmg naaygcnwsn 360
ytncargcnc argtngtnyt nwsnttycar gcntayccna cngcnmgntg ygtnytnytn 420
gargtncarg tnccngcngc nytngtncar ttyggncarw sngtnggnws ngtngtntay 480
```

gaytgyttyg argcngcnyt nggnwsngar gtnmgnatht ggwsntayac ncarccnmgn 540
taygaraarg arytnaayca yacncarcar ytnccngayt gymgnggnyt ngargtntgg 600
aaywsnathc cnwsntgytg ggcnytnccn tggytnaayg tnwsngcnga yggngayaay 660
gtncayytng tnytnaaygt nwsngargar carcayttyg gnytnwsnyt ntaytggaay 720
cargtncarg gnccnccnaa rccnmgntgg cayaaraayy tnacnggncc ncarathath 780
acnytnaayc ayacngayyt ngtnccntgy ytntgyathc argtntggcc nytngarccn 840
gaywsngtnm gnacnaayat htgyccntty mgngargayc cnmgngcnca ycaraayytn 900
tggcargcng cnmgnytnmg nytnytnacn ytncarwsnt ggytnytnga ygcnccntgy 960
wsnytnccng cngargcngc nytntgytgg mgngcnccng gnggngaycc ntgycarccn 1020
ytngtnccnc cnytnwsntg ggaraaygtn acngtngayg tnaaywsnws ngaraarytn 1080
carytncarg artgyytntg ggcngaywsn ytnggnccny tnaargayga ygtnytnytn 1140
ytngaracnm gnggnccnca rgayaaymgn wsnytntgyg cnytngarcc nwsnggntgy 1200
acnwsnytnc cnwsnaargc nwsnacnmgn gcngcnmgny tnggngarta yytnytncar 1260
gayytncarw snggncartg yytncarytn tgggaygayg ayytnggngc nytntgggcn 1320
tgyccnatgg ayaartayat hcayaarmgn tgggcnytng tntggytngc ntgyytnytn 1380
ttygcngcng cnytnwsnyt nathytnytn ytnaaraarg aycaygcnaa rggntggytn 1440
mgnytnytna arcargaygt nmgnwsnggn gcngcngcnm gnggnmgngc ngcnytnytn 1500
ytntaywsng cngaygayws nggnttygar mgnytngtng gngcnytngc nwsngcnytn 1560
tgycarytnc cnytnmgngt ngcngtngay ytntggwsnm gnmgngaryt nwsngcncar 1620
ggnccngtng cntggttyca ygcncarmgn mgncaracny tncargargg nggngtngtn 1680
gtnytnytnt tywsnccngg ngcngtngcn ytntgywsng artggytnca rgayggngtn 1740
wsnggnccng gngcncaygg nccncaygay gcnttymgng cnwsnytnws ntgygtnytn 1800
ccngayttyy tncarggnmg ngcnccnggn wsntaygtng gngcntgytt ygaymgnytn 1860
ytncayccng aygcngtncc ngcnytntty mgnacngtnc cngtnttyac nytnccnwsn 1920
carytnccng ayttyytngg ngcnytncar carccnmgng cnccnmgnws nggnmgnytn 1980
cargarmgng cngarcargt nwsnmgngcn ytncarccng cnytngayws ntayttycay 2040
ccnccnggna cnwsngcncc nggnmgnggn gtnggnccng gngcnggncc nggngcnggn 2100
gayggnacn 2109

Rodent, e.g., mouse, embodiment (see SEQ ID NO: 10 and 11). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

```
ccaaatcgaa agcacgggag ctgatactgg gcctggagtc caggctcact ggagtgggga 60

agcatggctg gagaggaatt ctagcccttg ctctctccca gggacacggg gctgattgtc 120

agcaggggcg aggggtctgc ccccccttgg gggggcagga cggggcctca ggcctgggtg 180

ctgtccggca cctggaag atg cct gtg tcc tgg ttc ctg ctg tcc ttg gca   231
                    Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala
                    -20                 -15                 -10

ctg ggc cga aac cct gtg gtc gtc tct ctg gag aga ctg atg gag cct   279
Leu Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro
                -5                  -1   1               5

cag gac act gca cgc tgc tct cta ggc ctc tcc tgc cac ctc tgg gat   327
Gln Asp Thr Ala Arg Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp
        10                  15                  20

ggt gac gtg ctc tgc ctg cct gga agc ctc cag tct gcc cca ggc cct   375
Gly Asp Val Leu Cys Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro
    25                  30                  35

gtg cta gtg cct acc cgc ctg cag acg gag ctg gtg ctg agg tgt cca   423
Val Leu Val Pro Thr Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro
40                  45                  50                  55

cag aag aca gat tgc gcc ctc tgt gtc cgt gtg gtg gtc cac ttg gcc   471
Gln Lys Thr Asp Cys Ala Leu Cys Val Arg Val Val Val His Leu Ala
                60                  65                  70

gtg cat ggg cac tgg gca gag cct gaa gaa gct gga aag tct gat tca   519
Val His Gly His Trp Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser
            75                  80                  85

gaa ctc cag gag tct agg aac gcc tct ctc cag gcc cag gtg gtg ctc   567
Glu Leu Gln Glu Ser Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu
        90                  95                  100

tcc ttc cag gcc tac ccc atc gcc cgc tgt gcc ctg ctg gag gtc cag   615
Ser Phe Gln Ala Tyr Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln
    105                 110                 115

gtg ccc gct gac ctg gtg cag cct ggt cag tcc gtg ggt tct gcg gta   663
Val Pro Ala Asp Leu Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val
120                 125                 130                 135

ttt gac tgt ttc gag gct agt ctt ggg gct gag gta cag atc tgg tcc   711
Phe Asp Cys Phe Glu Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser
                140                 145                 150

tac acg aag ccc agg tac cag aaa gag ctc aac ctc aca cag cag ctg   759
Tyr Thr Lys Pro Arg Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu
            155                 160                 165
```

```
cct gac tgc agg ggt ctt gaa gtc cgg gac agc atc cag agc tgc tgg    807
Pro Asp Cys Arg Gly Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp
        170                 175                 180

gtc ctg ccc tgg ctc aat gtg tct aca gat ggt gac aat gtc ctt ctg    855
Val Leu Pro Trp Leu Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu
    185                 190                 195

aca ctg gat gtc tct gag gag cag gac ttt agc ttc tta ctg tac ctg    903
Thr Leu Asp Val Ser Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu
200                 205                 210                 215

cgt cca gtc ccg gat gct ctc aaa tcc ttg tgg tac aaa aac ctg act    951
Arg Pro Val Pro Asp Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr
                220                 225                 230

gga cct cag aac att act tta aac cac aca gac ctg gtt ccc tgc ctc    999
Gly Pro Gln Asn Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu
            235                 240                 245

tgc att cag gtg tgg tcg cta gag cca gac tct gag agg gtc gaa ttc    1047
Cys Ile Gln Val Trp Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe
        250                 255                 260

tgc ccc ttc cgg gaa gat ccc ggt gca cac agg aac ctc tgg cac ata    1095
Cys Pro Phe Arg Glu Asp Pro Gly Ala His Arg Asn Leu Trp His Ile
    265                 270                 275

gcc agg ctg cgg gta ctg tcc cca ggg gta tgg cag cta gat gcg cct    1143
Ala Arg Leu Arg Val Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro
280                 285                 290                 295

tgc tgt ctg ccg ggc aag gta aca ctg tgc tgg cag gca cca gac cag    1191
Cys Cys Leu Pro Gly Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln
                300                 305                 310

agt ccc tgc cag cca ctt gtg cca cca gtg ccc cag aag aac gcc act    1239
Ser Pro Cys Gln Pro Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr
            315                 320                 325

gtg aat gag cca caa gat ttc cag ttg gtg gca ggc cac ccc aac ctc    1287
Val Asn Glu Pro Gln Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu
        330                 335                 340

tgt gtc cag gtg agc acc tgg gag aag gtt cag ctg caa gcg tgc ttg    1335
Cys Val Gln Val Ser Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Leu
    345                 350                 355

tgg gct gac tcc ttg ggg ccc ttc aag gat gat atg ctg tta gtg gag    1383
Trp Ala Asp Ser Leu Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu
360                 365                 370                 375

atg aaa acc ggc ctc aac aac aca tca gtc tgt gcc ttg gaa ccc agt    1431
Met Lys Thr Gly Leu Asn Asn Thr Ser Val Cys Ala Leu Glu Pro Ser
                380                 385                 390

ggc tgt aca cca ctg ccc agc atg gcc tcc acg aga gct gct cgc ctg    1479
Gly Cys Thr Pro Leu Pro Ser Met Ala Ser Thr Arg Ala Ala Arg Leu
            395                 400                 405
```

gga gag gag ttg ctg caa gac ttc cga tca cac cag tgt atg cag ctg 1527
Gly Glu Glu Leu Leu Gln Asp Phe Arg Ser His Gln Cys Met Gln Leu
410 415 420

tgg aac gat gac aac atg gga tcg cta tgg gcc tgc ccc atg gac aag 1575
Trp Asn Asp Asp Asn Met Gly Ser Leu Trp Ala Cys Pro Met Asp Lys
425 430 435

tac atc cac agg cgc tgg gtc cta gta tgg ctg gcc tgc cta ctc ttg 1623
Tyr Ile His Arg Arg Trp Val Leu Val Trp Leu Ala Cys Leu Leu Leu
440 445 450 455

gct gcg gcg ctt ttc ttc ttc ctc ctt cta aaa aag gac cgc agg aaa 1671
Ala Ala Ala Leu Phe Phe Phe Leu Leu Leu Lys Lys Asp Arg Arg Lys
460 465 470

gcg gcc cgt ggc tcc cgc acg gcc ttg ctc ctc cac tcc gcc gac gga 1719
Ala Ala Arg Gly Ser Arg Thr Ala Leu Leu Leu His Ser Ala Asp Gly
475 480 485

gcg ggc tac gag cgc ctg gtg gga gca ctg gcg tcc gcg ttg agc cag 1767
Ala Gly Tyr Glu Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Ser Gln
490 495 500

atg cca ctg cgc gtg gcc gtg gac ctg tgg agc cgc cgc gag ctg agc 1815
Met Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser
505 510 515

gcg cac gga gcc cta gcc tgg ttc cac cac cag cga cgc cgt atc ctg 1863
Ala His Gly Ala Leu Ala Trp Phe His His Gln Arg Arg Arg Ile Leu
520 525 530 535

cag gag ggt ggc gtg gta atc ctt ctc ttc tcg ccc gcg gcc gtg gcg 1911
Gln Glu Gly Gly Val Val Ile Leu Leu Phe Ser Pro Ala Ala Val Ala
540 545 550

cag tgt cag cag tgg ctg cag ctc cag aca gtg gag ccc ggg ccg cat 1959
Gln Cys Gln Gln Trp Leu Gln Leu Gln Thr Val Glu Pro Gly Pro His
555 560 565

gac gcc ctc gcc gcc tgg ctc agc tgc gtg cta ccc gat ttc ctg caa 2007
Asp Ala Leu Ala Ala Trp Leu Ser Cys Val Leu Pro Asp Phe Leu Gln
570 575 580

ggc cgg gcg acc ggc cgc tac gtc ggg gtc tac ttc gac ggg ctg ctg 2055
Gly Arg Ala Thr Gly Arg Tyr Val Gly Val Tyr Phe Asp Gly Leu Leu
585 590 595

cac cca gac tct gtg ccc tcc ccg ttc cgc gtc gcc ccg ctc ttc tcc 2103
His Pro Asp Ser Val Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser
600 605 610 615

ctg ccc tcg cag ctg ccg gct ttc ctg gat gca ctg cag gga ggc tgc 2151
Leu Pro Ser Gln Leu Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys
620 625 630

```
tcc act tcc gcg ggg cga ccc gcg gac cgg gtg gaa cga gtg acc cag     2199
Ser Thr Ser Ala Gly Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln
            635                 640                 645

gcg ctg cgg tcc gcc ctg gac agc tgt act tct agc tcg gaa gcc cca     2247
Ala Leu Arg Ser Ala Leu Asp Ser Cys Thr Ser Ser Ser Glu Ala Pro
        650                 655                 660

ggc tgc tgc gag gaa tgg gac ctg gga ccc tgc act aca cta gaa         2292
Gly Cys Cys Glu Glu Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
    665                 670                 675

taaaagccga tacagtattc ct                                            2314
```

```
MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDVLCLPGSLQSAPGPVLVPTRLQTELVL
RCPQKTDCALCVRVVVHLAVHGHWAEPEEAGKSDSELQESRNASLQAQVVLSFQAYPIARCALLEVQVPADL
VQPGQSVGSAVFDCFEASLGAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLNVSTDGDN
VLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFRE
DPGAHRNLWHIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGH
PNLCVQVSTWEKVQLQACLWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMASTRAARLGEELL
QDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALFFFLLLKKDRRKAARGSRTALLLHS
ADGAGYERLVGALASALSQMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQEGGVVILLFSPAAVAQCQQW
LQLQTVEPGPHDALAAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSLPSQLPAFLDALQ
GGCSTSAGRPADRVERVTQALRSALDSCTSSSEAPGCCEEWDLGPCTTLE.
```

Reverse translation of rodent, e.g., mouse, DCRS7 (SEQ ID NO: 12):

```
atgccngtnw sntggttyyt nytnwsnytn gcnytnggnm gnaayccngt ngtngtnwsn 60
ytngarmgny tnatggarcc ncargayacn gcnmgntgyw snytnggnyt nwsntgycay 120
ytntgggayg gngaygtnyt ntgyytnccn ggnwsnytnc arwsngcncc nggnccngtn 180
ytngtnccna cnmgnytnca racngarytn gtnytnmgnt gyccncaraa racngaytgy 240
gcnytntgyg tnmgngtngt ngtncayytn gcngtncayg gncaytgggc ngarccngar 300
gargcnggna arwsngayws ngarytncar garwsnmgna aygcnwsnyt ncargcncar 360
gtngtnytnw snttycargc ntayccnath gcnmgntgyg cnytnytnga rgtncargtn 420
ccngcngayy tngtncarcc nggncarwsn gtnggnwsng cngtnttyga ytgyttygar 480
gcnwsnytng gngcngargt ncarathtgg wsntayacna arccnmgnta ycaraargar 540
ytnaayytna cncarcaryt nccngaytgy mgnggnytng argtnmgnga ywsnathcar 600
wsntgytggg tnytnccntg gytnaaygtn wsnacngayg gngayaaygt nytnytnacn 660
ytngaygtnw sngargarca rgayttywsn ttyytnytnt ayytnmgncc ngtnccngay 720
gcnytnaarw snytntggta yaaraayytn acnggnccnc araayathac nytnaaycay 780
acngayytng tnccntgyyt ntgyathcar gtntggwsny tngarccnga ywsngarmgn 840
gtngarttyt gyccnttymg ngargayccn ggngcncaym gnaayytntg gcayathgcn 900
mgnytnmgng tnytnwsncc nggngtntgg carytngayg cnccntgytg yytnccnggn 960
```

```
aargtnacny tntgytggca rgcnccngay carwsnccnt gycarccnyt ngtnccnccn 1020
gtnccncara araaygcnac ngtnaaygar ccncargayt tycarytngt ngcnggncay 1080
ccnaayytnt gygtncargt nwsnacntgg garaargtnc arytncargc ntgyytntgg 1140
gcngaywsny tnggnccntt yaargaygay atgytnytng tngaratgaa racnggnytn 1200
aayaayacnw sngtntgygc nytngarccn wsnggntgya cnccnytncc nwsnatggcn 1260
wsnacnmgng cngcnmgnyt nggngargar ytnytncarg ayttymgnws ncaycartgy 1320
atgcarytnt ggaaygayga yaayatgggn wsnytntggg cntgyccnat ggayaartay 1380
athcaymgnm gntgggtnyt ngtntggytn gcntgyytny tnytngcngc ngcnytntty 1440
ttyttyytny tnytnaaraa rgaymgnmgn aargcngcnm gnggnwsnmg nacngcnytn 1500
ytnytncayw sngcngaygg ngcnggntay garmgnytng tnggngcnyt ngcnwsngcn 1560
ytnwsncara tgccnytnmg ngtngcngtn gayytntggw snmgnmgnga rytnwsngcn 1620
cayggngcny tngcntggtt ycaycaycar mgnmgnmgna thytncarga rggnggngtn 1680
gtnathytny tnttywsncc ngcngcngtn gcncartgyc arcartggyt ncarytncar 1740
acngtngarc cnggnccnca ygaygcnytn gcngcntggy tnwsntgygt nytnccngay 1800
ttyytncarg gnmgngcnac nggnmgntay gtnggngtnt ayttygaygg nytnytncay 1860
ccngaywsng tnccnwsncc nttymgngtn gcnccnytnt tywsnytncc nwsncarytn 1920
ccngcnttyy tngaygcnyt ncarggnggn tgywsnacnw sngcnggnmg nccngcngay 1980
mgngtngarm gngtnacnca rgcnytnmgn wsngcnytng aywsntgyac nwsnwsnwsn 2040
gargcnccng gntgytgyga rgartgggay ytnggnccnt gyacnacnyt ngar       2094
```

Table 3: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiments (DCRS8). Primate, e.g., human, embodiment (see SEQ ID NO: 13 and 14). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

```
cccacgcntc cgggccagca gcgggcggcc ggggcgcaga gaacggcctg gctgggcgag 60

cgcacggcc atg gcc ccg tgg ctg cag ctc tgc tcc gtc ttc ttt acg gtc 111
          Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val
              -15                 -10                  -5

aac gcc tgc ctc aac ggc tcg cag ctg gct gtn gcc gct ggc ggg tcc   159
Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Xaa Ala Ala Gly Gly Ser
     -1   1               5                  10

ggc cgc gcg cng ggc gcc gac acc tgt agc tgg ang gga gtg ggg cca   207
Gly Arg Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro
 15                  20                  25                  30
```

```
gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa tat gac aat   255
Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn
                 35                  40                  45

tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att gct gac gcc   303
Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala
             50                  55                  60

cag aat atc acc atc agc cag tat gct tgc cat gac caa gtg gca gtc   351
Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val
         65                  70                  75

acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc ctg aaa gga   399
Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly
     80                  85                  90

ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga cag ngc caa   447
Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln
 95                 100                 105                 110

caa ctg att cta aag gat ccg aag cag ntc aac agt agc ttc aaa aga   495
Gln Leu Ile Leu Lys Asp Pro Lys Gln Xaa Asn Ser Ser Phe Lys Arg
                115                 120                 125

act gga atg gaa tct caa cct ttn ctg aat atg aaa ttt gaa acg gat   543
Thr Gly Met Glu Ser Gln Pro Xaa Leu Asn Met Lys Phe Glu Thr Asp
            130                 135                 140

tat ttc gta agg ttg tcc ttt tcc ttc att aaa aac gaa agc aat tac   591
Tyr Phe Val Arg Leu Ser Phe Ser Phe Ile Lys Asn Glu Ser Asn Tyr
        145                 150                 155

cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg ttg tta cag ccg   639
His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro
    160                 165                 170

gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg aac ctg aac atc   687
Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile
175                 180                 185                 190

agc cag cat ggc tcg gac atg cag gtg tcc ttc gac cac gca ccg cac   735
Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His
                195                 200                 205

aac ttc ggc ttc cgt ttc ttc tat ctt cac tac aag ctc aag cac gaa   783
Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu
            210                 215                 220

gga cct ttc aag cga aag acc tgt aag cag gag caa act aca gag atg   831
Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met
        225                 230                 235

acc agc tgc ctc ctt caa aat gtt tct cca ggg gat tat ata att gag   879
Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu
    240                 245                 250
```

```
ctg gtg gat gac act aac aca aca aga aaa gtg atg cat tat gcc tta     927
Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu
255                 260                 265                 270

aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga gcc gtg gcc atc     975
Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile
                275                 280                 285

aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg ctc ttc act gtg    1023
Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val
            290                 295                 300

atg tgc cgc aag aag caa caa gaa aat ata tat tca cat tta gat gaa    1071
Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu
        305                 310                 315

gag agc tct gag tct tcc aca tac act gca gca ctc cca aga gag agg    1119
Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg
    320                 325                 330

ctc cgg ccg cgg ccg aag gtc ttt ctc tgc tat tcc agt aaa gat ggc    1167
Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly
335                 340                 345                 350

cag aat cac atg aat gtc gtc cag tgt ttc gcc tac ttc ctc cag gac    1215
Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp
                355                 360                 365

ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa gac ttc agc ctc    1263
Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu
            370                 375                 380

tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag atc cac gag tcc    1311
Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser
        385                 390                 395

cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag tac ttt gtg gac    1359
Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp
    400                 405                 410

aag aag aac tac aaa cac aaa gga ggt ggc cga ggc tcg ggg aaa gga    1407
Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly
415                 420                 425                 430

gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa aag ctc cgc cag    1455
Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln
                435                 440                 445

gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt atc gcc gtc tac    1503
Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr
            450                 455                 460
ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc cta gac ctg agt    1551
Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser
        465                 470                 475

acc aag tac aga ctc atg gac aat ctt cct cag ctc tgt tcc cac ctg    1599
Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu
    480                 485                 490
```

```
cac tcc cga gac cac ggc ctc cag gag ccg ggg cag cac acg cga cag   1647
His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln
495                 500                 505                 510

ggc agc aga agg aac tac ttc cgg agc aag tca ggc cgg tcc cta tac   1695
Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr
                515                 520                 525

gtc gcc att tgc aac atg cac cag ttt att gac gag gag ccc gac tgg   1743
Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp
            530                 535                 540

ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca ctg cgc tac cgg   1791
Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg
        545                 550                 555

gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt tta aat gat gtc   1839
Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val
    560                 565                 570

atg tgc aaa cca ggg cct gag agt gac ttc tgc cta aag gta gag gcg   1887
Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala
575                 580                 585                 590

gct gtt ctt ggg gca acc gga cca gcc gac tcc cag cac gag agt cag   1935
Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln
                595                 600                 605

cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct gcc ctt gac ggt   1983
His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly
            610                 615                 620

agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa gcc ggc agc ccc   2031
Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro
        625                 630                 635

tcg gac atg ccg cgg gac tca ggc atc tat gac tcg tct gtg ccc tca   2079
Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser
    640                 645                 650

tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg acg gac cag aca   2127
Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr
655                 660                 665                 670

gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct tca ggc ctg ggt   2175
Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly
                675                 680                 685

gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc tct tct ggg tca   2223
Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser
            690                 695                 700

tgc aaa gca gat ctt ggt tgc cgc agc tac act gat gaa ctc cac gcg   2271
Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala
        705                 710                 715

gtc gcc cct ttg taacaaaacg aaagagtcta agcattgcca ctttagctgc       2323
Val Ala Pro Leu
    720
```

tgcctccctc tgattcccca gctcatctcc ctggttgcat ggcccacttg gagctgaggt 2383

ctcatacaag gatatttgga gtgaaatgct ggccagtact tgttctccct tgccccaacc 2443

ctttaccgga tatcttgaca aactctccaa ttttctaaaa tgatatggag ctctgaaagg 2503

catgtccata aggtctgaca acagcttgcc aaatttggtt agtccttgga tcagagcctg 2563

ttgtgggagg tagggaggaa atatgtaaag aaaaacagga agatacctgc actaatcatt 2623

cagacttcat tgagctctgc aaactttgcc tgtttgctat tggctacctt gatttgaaat 2683

gctttgtgaa aaaaggcact tttaacatca tagccacaga aatcaagtgc cagtctatct 2743

ggaatccatg ttgtattgca gataatgttc tcatttattt ttg 2786

MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRAXGADTCSWXGVGPASRNSGLYNITFKYDNCTTYLNPVGK
HVIADAQNITISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQXQQLILKDPKQXNSSFKRTG
MESQPXLNMKFETDYFVRLSFSFIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVS
FDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKP
VHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLC
YSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKK
NYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLP
QLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREP
VLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHT
VKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCK
ADLGCRSYTDELHAVAPL.

Reverse translation of primate, e.g., human, DCRS8 (SEQ ID NO: 15):

atggcnccnt ggytncaryt ntgywsngtn ttyttyacng tnaaygcntg yytnaayggn 60

wsncarytng cngtngcngc nggnggnwsn ggnmgngcnn nnggngcnga yacntgywsn 120

tggnnnggng tnggnccngc nwsnmgnaay wsnggnytnt ayaayathac nttyaartay 180

gayaaytgya cnacntayyt naayccngtn ggnaarcayg tnathgcnga ygcncaraay 240

athacnathw sncartaygc ntgycaygay cargtngcng tnacnathyt ntggwsnccn 300

ggngcnytng gnathgartt yytnaarggn ttymgngtna thytngarga rytnaarwsn 360

garggnmgnc arnnncarca rytnathytn aargayccna arcarnnnaa ywsnwsntty 420

aarmgnacng gnatggarws ncarccnnnn ytnaayatga arttygarac ngaytaytty 480

gtnmgnytnw snttywsntt yathaaraay garwsnaayt aycayccntt yttyttymgn 540

acnmgngcnt gygayytnyt nytncarccn gayaayytng cntgyaarcc nttytggaar 600

ccnmgnaayy tnaayathws ncarcayggn wsngayatgc argtnwsntt ygaycaygcn 660

ccncayaayt tyggnttymg nttyttytay ytncaytaya arytnaarca ygarggnccn 720

ttyaarmgna aracntgyaa rcargarcar acnacngara tgacnwsntg yytnytncar 780

aaygtnwsnc cnggngayta yathathgar ytngtngayg ayacnaayac nacnmgnaar 840

```
gtnatgcayt aygcnytnaa rccngtncay wsnccntggg cnggnccnat hmgngcngtn 900
gcnathacng tnccnytngt ngtnathwsn gcnttygcna cnytnttyac ngtnatgtgy 960
mgnaaraarc arcargaraa yathtaywsn cayytngayg argarwsnws ngarwsnwsn 1020
acntayacng cngcnytncc nmgngarmgn ytnmgnccnm gnccnaargt nttyytntgy 1080
taywsnwsna argayggnca raaycayatg aaygtngtnc artgyttygc ntayttyytn 1140
cargayttyt gyggntgyga rgtngcnytn gayytntggg argayttyws nytntgymgn 1200
garggncarm gngartgggt nathcaraar athcaygarw sncarttyat hathgtngtn 1260
tgywsnaarg gnatgaarta yttygtngay aaraaraayt ayaarcayaa rggnggnggn 1320
mgnggnwsng gnaarggnga rytnttyytn gtngcngtnw sngcnathgc ngaraarytn 1380
mgncargcna arcarwsnws nwsngcngcn ytnwsnaart tyathgcngt ntayttygay 1440
taywsntgyg arggngaygt nccnggnath ytngayytnw snacnaarta ymgnytnatg 1500
gayaayytnc cncarytntg ywsncayytn caywsnmgng aycayggnyt ncargarccn 1560
ggncarcaya cnmgncargg nwsnmgnmgn aaytayttym gnwsnaarws nggnmgnwsn 1620
ytntaygtng cnathtgyaa yatgcaycar ttyathgayg argarccnga ytggttygar 1680
aarcarttyg tnccnttyca yccnccnccn ytnmgntaym gngarccngt nytngaraar 1740
ttygaywsng gnytngtnyt naaygaygtn atgtgyaarc cnggnccnga rwsngaytty 1800
tgyytnaarg tngargcngc ngtnytnggn gcnacnggnc cngcngayws ncarcaygar 1860
wsncarcayg gnggnytnga ycargayggn gargcnmgnc cngcnytnga yggnwsngcn 1920
gcnytncarc cnytnytnca yacngtnaar gcnggnwsnc cnwsngayat gccnmgngay 1980
wsnggnatht aygaywsnws ngtnccnwsn wsngarytnw snytnccnyt natggarggn 2040
ytnwsnacng aycaracnga racnwsnwsn ytnacngarw sngtnwsnws nwsnwsnggn 2100
ytnggngarg argarccncc ngcnytnccn wsnaarytny tnwsnwsngg nwsntgyaar 2160
gcngayytng gntgymgnws ntayacngay garytncayg cngtngcncc nytn       2214
```

Table 4: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiments (DCRS9). Primate, e.g., human, embodiment (see SEQ ID NO: 16 and 17). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

```
atg ggg agc tcc aga ctg gca gcc ctg ctc ctg cct ctc ctc ctc ata    48
Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile
            -20                 -15                 -10
```

```
gtc atc gac ctc tct gac tct gct ggg att ggc ttt cgc cac ctg ccc    96
Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro
         -5                  -1   1               5

cac tgg aac acc cgc tgt cct ctg gcc tcc cac acg gaa gtt ctg cct   144
His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro
 10                  15                  20                  25

ata tcc ctt gcc gca cct ggt ggg ccc tct tct cca caa agc ctt ggt   192
Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly
                 30                  35                  40

gtg tgc gag tct ggc act gtt ccc gct gtt tgt gcc agc atc tgc tgt   240
Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys
             45                  50                  55

cag gtg gct cag gtc ttc aac ggg gcc tct tcc acc tcc tgg tgc aga   288
Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg
         60                  65                  70

aat cca aaa agt ctt cca cat tca agt tct ata gga gac aca aga tgc   336
Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys
     75                  80                  85

cag cac ctg ctc aga gga agc tgc tgc ctc gtc gtc acc tgt ctg aga   384
Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg
 90                  95                 100                 105

aga gcc atc aca ttt cca tcc cct ccc cag aca tct ccc aca agg gac   432
Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp
                110                 115                 120

ttc gct cta aaa gga ccc aac ctt cgg atc cag aga cat ggg aaa gtc   480
Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val
            125                 130                 135

ttc cca gat tgg act cac aaa ggc atg gag gtg ggc act ggg tac aac   528
Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn
        140                 145                 150

agg aga tgg gtt cag ctg agt ggt gga ccc gag ttc tcc ttt gat ttg   576
Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu
    155                 160                 165

ctg cct gag gcc cgg gct att cgg gtg acc ata tct tca ggc cct gag   624
Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu
170                 175                 180                 185

gtc agc gtg cgt ctt tgt cac cag tgg gca ctg gag tgt gaa gag ctg   672
Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu
                190                 195                 200

agc agt ccc tat gat gtc cag aaa att gtg tct ggg ggc cac act gta   720
Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val
            205                 210                 215

gag ctg cct tat gaa ttc ctt ctg ccc tgt ctg tgc ata gag gca tcc   768
Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser
        220                 225                 230
```

```
tac ctg caa gag gac act gtg agg cgc aaa aaa tgt ccc ttc cag agc    816
Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser
    235                 240                 245

tgg cca gaa gcc tat ggc tcg gac ttc tgg aag tca gtg cac ttc act    864
Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr
250                 255                 260                 265

gac tac agc cag cac act cag atg gtc atg gcc ctg aca ctc cgc tgc    912
Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys
                270                 275                 280

cca ctg aag ctg gaa gct gcc ctc tgc cag agg cac gac tgg cat acc    960
Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr
            285                 290                 295

ctt tgc aaa gac ctc ccg aat gcc acg gct cga gag tca gat ggg tgg    1008
Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp
        300                 305                 310

tat gtt ttg gag aag gtg gac ctg cac ccc cag ctc tgc ttc aag gta    1056
Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val
    315                 320                 325

caa cca tgg ttc tct ttt gga aac agc agc cat gtt gaa tgc ccc cac    1104
Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His
330                 335                 340                 345

cag act ggg tct ctc aca tcc tgg aat gta agc atg gat acc caa gcc    1152
Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala
                350                 355                 360

cag cag ctg att ctt cac ttc tcc tca aga atg cat gcc acc ttc agt    1200
Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser
            365                 370                 375

gct gcc tgg agc ctc cca ggc ttg ggg cag gac act ttg gtg ccc ccc    1248
Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro
        380                 385                 390

gtg tac act gtc agc cag gtg tgg cgg tca gat gtc cag ttt gcc tgg    1296
Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp
    395                 400                 405

aag cac ctc ttg tgt cca gat gtc tct tac aga cac ctg ggg ctc ttg    1344
Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu
410                 415                 420                 425

atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg gcc    1392
Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala
                430                 435                 440

ctc acc tgc cgg cgc cca cag tca ggc ccg ggc cca gcg cgg cca gtg    1440
Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val
            445                 450                 455
```

```
ctc ctc ctg cac gcg gcg gac tcg gag gcg cag cgg cgc ctg gtg gga    1488
Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly
        460                 465                 470

gcg ctg gct gaa ctg cta cgg gca gcg ctg ggc ggc ggg cgc gac gtg    1536
Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val
    475                 480                 485

atc gtg gac ctg tgg gag ggg agg cac gtg gcg cgc gtg ggc ccg ctg    1584
Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu
490                 495                 500                 505

ccg tgg ctc tgg gcg gcg cgg acg cgc gta gcg cgg gag cag ggc act    1632
Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr
                510                 515                 520

gtg ctg ctg ctg tgg agc ggc gcc gac ctt cgc ccg gtc agc ggc ccc    1680
Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro
            525                 530                 535

gac ccc cgc gcc gcg ccc ctg ctc gcc ctg ctc cac gct gcc ccg cgc    1728
Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg
        540                 545                 550

ccg ctg ctg ctg ctc gct tac ttc agt cgc ctc tgc gcc aag ggc gac    1776
Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp
    555                 560                 565

atc ccc ccg ccg ctg cgc gcc ctg ccg cgc tac cgc ctg ctg cgc gac    1824
Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp
570                 575                 580                 585

ctg ccg cgt ctg ctg cgg gcg ctg gac gcg cgg cct ttc gca gag gcc    1872
Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala
                590                 595                 600

acc agc tgg ggc cgc ctt ggg gcg cgg cag cgc agg cag agc cgc cta    1920
Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu
            605                 610                 615

gag ctg tgc agc cgg ctc gaa cga gag gcc gcc cga ctt gca gac cta    1968
Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu
        620                 625                 630

ggt tgagcagagc tccaccgcag tcccgggtgt ctgcggccgc t                  2012
Gly
```

```
MGSSRLAALLLPLLLIVIDLSDSAGIGFRHLPHWNTRCPLASHTEVLPISLAAPGGPSSPQSLGVCESGTVP
AVCASICCQVAQVFNGASSTSWCRNPKSLPHSSSIGDTRCQHLLRGSCCLVVTCLRRAITFPSPPQTSPTRD
FALKGPNLRIQRHGKVFPDWTHKGMEVGTGYNRRWVQLSGGPEFSFDLLPEARAIRVTISSGPEVSVRLCHQ
WALECEELSSPYDVQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFT
DYSQHTQMVMALTLRCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKVQPWFSFGN
SSHVECPHQTGSLTSWNVSMDTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQVWRSDVQFAW
KHLLCPDVSYRHLGLLILALLALLTLLGVVLALTCRRPQSGPGPARPVLLLHAADSEAQRRLVGALAELLRA
ALGGGRDVIVDLWEGRHVARVGPLPWLWAARTRVAREQGTVLLLWSGADLRPVSGPDPRAAPLLALLHAAPR
PLLLLAYFSRLCAKGDIPPPLRALPRYRLLRDLPRLLRALDARPFAEATSWGRLGARQRRQSRLELCSRLER
EAARLADLG.
```

Reverse translation of primate, e.g., human, DCRS9 (SEQ ID NO: 18):

atgggnwsnw snmgnytngc ngcnytnytn ytnccnytny tnytnathgt nathgayytn 60
wsngaywsng cnggnathgg nttymgncay ytnccncayt ggaayacnmg ntgyccnytn 120
gcnwsncaya cngargtnyt nccnathwsn ytngcngcnc cnggnggncc nwsnwsnccn 180
carwsnytng gngtntgyga rwsnggnacn gtnccngcng tntgygcnws nathtgytgy 240
cargtngcnc argtnttyaa yggngcnwsn wsnacnwsnt ggtgymgnaa yccnaarwsn 300
ytnccncayw snwsnwsnat hggngayacn mgntgycarc ayytnytnmg nggnwsntgy 360
tgyytngtng tnacntgyyt nmgnmgngcn athacnttyc cnwsnccncc ncaracnwsn 420
ccnacnmgng ayttygcnyt naarggnccn aayytnmgna thcarmgnca yggnaargtn 480
ttyccngayt ggacncayaa rggnatggar gtnggnacng gntayaaymg nmgntgggtn 540
carytnwsng gnggnccnga rttywsntty gayytnytnc cngargcnmg ngcnathmgn 600
gtnacnathw snwsnggncc ngargtnwsn gtnmgnytnt gycaycartg ggcnytngar 660
tgygargary tnwsnwsncc ntaygaygtn caraarathg tnwsnggngg ncayacngtn 720
garytnccnt aygarttyyt nytnccntgy ytntgyathg argcnwsnta yytncargar 780
gayacngtnm gnmgnaaraa rtgyccntty carwsntggc cngargcnta yggnwsngay 840
ttytggaarw sngtncaytt yacngaytay wsncarcaya cncaratggt natggcnytn 900
acnytnmgnt gyccnytnaa rytngargcn gcnytntgyc armgncayga ytggcayacn 960
ytntgyaarg ayytnccnaa ygcnacngcn mgngarwsng ayggntggta ygtnytngar 1020
aargtngayy tncayccnca rytntgytty aargtncarc cntggttyws nttyggnaay 1080
wsnwsncayg tngartgycc ncaycaracn ggnwsnytna cnwsntggaa ygtnwsnatg 1140
gayacncarg cncarcaryt nathytncay ttywsnwsnm gnatgcaygc nacnttywsn 1200
gcngcntggw snytnccngg nytnggncar gayacnytng tnccnccngt ntayacngtn 1260
wsncargtnt ggmgnwsnga ygtncartty gcntggaarc ayytnytntg yccngaygtn 1320
wsntaymgnc ayytnggnyt nytnathytn gcnytnytng cnytnytnac nytnytnggn 1380
gtngtnytng cnytnacntg ymgnmgnccn carwsnggnc cnggnccngc nmgnccngtn 1440
ytnytnytnc aygcngcnga ywsngargcn carmgnmgny tngtnggngc nytngcngar 1500
ytnytnmgng cngcnytngg nggnggnmgn gaygtnathg tngayytntg ggarggnmgn 1560
caygtngcnm gngtnggncc nytnccntgg ytntgggcng cnmgnacnmg ngtngcnmgn 1620
garcarggna cngtnytnyt nytntggwsn ggngcngayy tnmgnccngt nwsnggnccn 1680

```
gayccnmgng cngcnccnyt nytngcnytn ytncaygcng cnccnmgncc nytnytnytn 1740
ytngcntayt tywsnmgnyt ntgygcnaar ggngayathc cnccnccnyt nmgngcnytn 1800
ccnmgntaym gnytnytnmg ngayytnccn mgnytnytnm gngcnytnga ygcnmgnccn 1860
ttygcngarg cnacnwsntg gggnmgnytn ggngcnmgnc armgnmgnca rwsnmgnytn 1920
garytntgyw snmgnytnga rmgngargcn gcnmgnytng cngayytngg n          1971
```

Rodent, e.g., mouse, embodiment (see SEQ ID NO: 19 and 20). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

```
cagctccggg ccaggccctg ctgccctctt gcagacagga aagacatggt ctctgcgccc 60

tgatcctaca gaagctc atg ggg agc ccc aga ctg gca gcc ttg ctc ctg     110
                   Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu
                                   -20                 -15

tct ctc ccg cta ctg ctc atc ggc ctc gct gtg tct gct cgg gtt gcc     158
Ser Leu Pro Leu Leu Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala
        -10                 -5                  -1   1

tgc ccc tgc ctg cgg agt tgg acc agc cac tgt ctc ctg gcc tac cgt     206
Cys Pro Cys Leu Arg Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg
 5                  10                  15                  20

gtg gat aaa cgt ttt gct ggc ctt cag tgg ggc tgg ttc cct ctc ttg     254
Val Asp Lys Arg Phe Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu
                25                  30                  35

gtg agg aaa tct aaa agt cct cct aaa ttt gaa gac tat tgg agg cac     302
Val Arg Lys Ser Lys Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His
            40                  45                  50

agg aca cca gca tcc ttc cag agg aag ctg cta ggc agc cct tcc ctg     350
Arg Thr Pro Ala Ser Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu
        55                  60                  65

tct gag gaa agc cat cga att tcc atc ccc tcc tca gcc atc tcc cac     398
Ser Glu Glu Ser His Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His
    70                  75                  80

aga ggc caa cgc acc aaa agg gcc cag cct tca gct gca gaa gga aga     446
Arg Gly Gln Arg Thr Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg
85                  90                  95                  100

gaa cat ctc cct gaa gca ggg tca caa aag tgt gga gga cct gaa ttc     494
Glu His Leu Pro Glu Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe
                105                 110                 115

tcc ttt gat ttg ctg ccc gag gtg cag gct gtt cgg gtg act att cct     542
Ser Phe Asp Leu Leu Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro
            120                 125                 130
```

```
gca ggc ccc aag gca cgt gtg cgc ctt tgt tat cag tgg gca ctg gaa     590
Ala Gly Pro Lys Ala Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu
        135                 140                 145

tgt gaa gac ttg agt agc cct ttt gat acc cag aaa att gtg tct gga     638
Cys Glu Asp Leu Ser Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly
    150                 155                 160

ggg cac act gta gac ctg cct tat gaa ttc ctt ctg ccc tgc atg tgc     686
Gly His Thr Val Asp Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys
165                 170                 175                 180

ata gag gcc tcc tac ctg caa gag gac act gtg agg cgc aaa agt gtc     734
Ile Glu Ala Ser Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val
                185                 190                 195

cct tcc aga gct ggc ctg aag ctt atg gct cag act tct ggc agt caa     782
Pro Ser Arg Ala Gly Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln
            200                 205                 210

tac gct tca ctg act aca gcc agc ac                                  808
Tyr Ala Ser Leu Thr Thr Ala Ser
        215                 220
```

MGSPRLAALLLSLPLLLIGLAVSARVACPCLRSWTSHCLLAYRVDKRFAGLQWGWFPLLVRKSKSPPKFEDY
WRHRTPASFQRKLLGSPSLSEESHRISIPSSAISHRGQRTKRAQPSAAEGREHLPEAGSQKCGGPEFSFDLL
PEVQAVRVTIPAGPKARVRLCYQWALECEDLSSPFDTQKIVSGGHTVDLPYEFLLPCMCIEASYLQEDTVRR
KSVPSRAGLKLMAQTSGSQYASLTTAS

Reverse translation of rodent, e.g., mouse, DCRS9 (SEQ ID NO: 21):

```
atgggnwsnc cnmgnytngc ngcnytnytn ytnwsnytnc cnytnytnyt nathggnytn 60
gcngtnwsng cnmgngtngc ntgyccntgy ytnmgnwsnt ggacnwsnca ytgyytnytn 120
gcntaymgng tngayaarmg nttygcnggn ytncartggg gntggttycc nytnytngtn 180
mgnaarwsna arwsnccncc naarttygar gaytaytggm gncaymgnac nccngcnwsn 240
ttycarmgna arytnytngg nwsnccnwsn ytnwsngarg arwsncaymg nathwsnath 300
ccnwsnwsng cnathwsnca ymgnggncar mgnacnaarm gngcncarcc nwsngcngcn 360
garggnmgng arcayytncc ngargcnggn wsncaraart gyggnggncc ngarttywsn 420
ttygayytny tnccngargt ncargcngtn mgngtnacna thccngcngg nccnaargcn 480
mgngtnmgny tntgytayca rtgggcnytn gartgygarg ayytnwsnws nccnttygay 540
acncaraara thgtnwsngg nggncayacn gtngayytnc cntaygartt yytnytnccn 600
tgyatgtgya thgargcnws ntayytncar gargayacng tnmgnmgnaa rwsngtnccn 660
wsnmgngcng gnytnaaryt natggcncar acnwsnggnw sncartaygc nwsnytnacn 720
acngcnwsn                                                        729
```

Table 5: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiments (DCRS10). Primate, e.g., human, embodiment (see SEQ ID NO: 22 and 23).

```
ttttgagcag aggcttccta ggctccgtag aaatttgcat acagcttcca cttcctgctt 60

cagagcctgt tcttctactt acctgggccc ggagaaggtg gagggagacg agaagccgcc 120

gagagccgac taccctccgg gcccagtctg tctgtccgtg gtggatctaa gaaactaga  179

atg aac cga agc att cct gtg gag gtt gat gaa tca gaa cca tac cca   227
Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
 1               5                  10                  15

agt cag ttg ctg aaa cca atc cca gaa tat tcc ccg gaa gag gaa tca   275
Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
            20                  25                  30

gaa cca cct gct cca aat ata agg aac atg gca ccc aac agc ttg tct   323
Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
        35                  40                  45

gca ccc aca atg ctt cac aat tcc tcc gga gac ttt tct caa gct cac   371
Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
    50                  55                  60

tca acc ctg aaa ctt gca aat cac cag cgg cct gta tcc cgg cag gtc   419
Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
65                  70                  75                  80

acc tgc ctg cgc act caa gtt ctg gag gac agt gaa gac agt ttc tgc   467
Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys
                85                  90                  95

agg aga cac cca ggc ctg ggc aaa gct ttc cct tct ggg tgc tct gca   515
Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala
            100                 105                 110

gtc agc gag cct gcg tct gag tct gtg gtt gga gcc ctc cct gca gag   563
Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu
        115                 120                 125

cat cag ttt tca ttt atg gaa aaa cgt aat caa tgg ctg gta tct cag   611
His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln
    130                 135                 140

ctt tca gcg gct tct cct gac act ggc cat gac tca gac aaa tca gac   659
Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp
145                 150                 155                 160

caa agt tta cct aat gcc tca gca gac tcc ttg ggc ggt agc cag gag   707
Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu
                165                 170                 175

atg gtg caa cgg ccc cag cct cac agg aac cga gca ggc ctg gat ctg   755
Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu
            180                 185                 190
```

cca acc ata gac acg gga tat gat tcc cag ccc cag gat gtc ctg ggc 803
Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly
195 200 205

atc agg cag ctg gaa agg ccc ctg ccc ctc acc tcc gtg tgt tac ccc 851
Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro
210 215 220

cag gac ctc ccc aga cct ctc agg tcc agg gag ttc cct cag ttt gaa 899
Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu
225 230 235 240

cct cag agg tat cca gca tgt gca cag atg ctg cct ccc aat ctt tcc 947
Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser
245 250 255

cca cat gct cca tgg aac tat cat tac cat tgt cct gga agt ccc gat 995
Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp
260 265 270

cac cag gtg cca tat ggc cat gac tac cct cga gca gcc tac cag caa 1043
His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln
275 280 285

gtg atc cag ccg gct ctg cct ggg cag ccc ctg cct gga gcc agt gtg 1091
Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val
290 295 300

aga ggc ctg cac cct gtg cag aag gtt atc ctg aat tat ccc agc ccc 1139
Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro
305 310 315 320

tgg gac caa gaa gag agg ccc gca cag aga gac tgc tcc ttt ccg ggg 1187
Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly
325 330 335

ctt cca agg cac cag gac cag cca cat cac cag cca cct aat aga gct 1235
Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala
340 345 350

ggt gct cct ggg gag tcc ttg gag tgc cct gca gag ctg aga cca cag 1283
Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln
355 360 365

gtt ccc cag cct ccg tcc cca gct gct gtg cct aga ccc cct agc aac 1331
Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn
370 375 380

cct cca gcc aga gga act cta aaa aca agc aat ttg cca gaa gaa ttg 1379
Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu
385 390 395 400

cgg aaa gtc ttt atc act tat tcg atg gac aca gct atg gag gtg gtg 1427
Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val
405 410 415

aaa ttc gtg aac ttt ttg ttg gta aat ggc ttc caa act gca att gac 1475
Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp
420 425 430

```
ata ttt gag gat aga atc cga ggc att gat atc att aaa tgg atg gag   1523
Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu
        435                 440                 445

cgc tac ctt agg gat aag acc gtg atg ata atc gta gca atc agc ccc   1571
Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro
    450                 455                 460

aaa tac aaa cag gac gtg gaa ggc gct gag tcg cag ctg gac gag gat   1619
Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp
465                 470                 475                 480

gag cat ggc tta cat act aag tac att cat cga atg atg cag att gag   1667
Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu
                485                 490                 495

ttc ata aaa caa gga agc atg aat ttc aga ttc atc cct gtg ctc ttc   1715
Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
            500                 505                 510

cca aat gct aag aag gag cat gtg ccc acc tgg ctt cag aac act cat   1763
Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
        515                 520                 525

gtc tac agc tgg ccc aag aat aaa aaa aac atc ctg ctg cgg ctg ctg   1811
Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
    530                 535                 540

aga gag gaa gag tat gtg gct cct cca cgg ggg cct ctg ccc acc ctt   1859
Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu
545                 550                 555                 560

cag gtg gtt ccc ttg tgacaccgtt catccccaga tcactgaggc caggccatgt   1914
Gln Val Val Pro Leu
                565

ttggggcctt gttctgacag cattctggct gaggctggtc ggtagcactc ctggctggtt 1974

tttttctgtt cctccccgag aggccctctg gcccccagga aacctgttgt gcagagctct 2034

tccccggaga cctccacaca ccctggcttt gaagtggagt ctgtgactgc tctgcattct 2094

ctgcttttaa aaaaaccatt gcaggtgcca gtgtcccata tgttcctcct gacagtttga 2154

tgtgtccatt ctgggcctct cagtgcttag caagtagata atgtaaggga tgtggcagca 2214

aatggaaatg actacaaaca ctctcctatc aatcacttca ggctactttt atgagttagc 2274

cagatgcttg tgtatcctca gaccaaactg attcatgtac aaataataaa atgtttactc 2334

ttttgtaaaa aaaaaaaaaa aaaaaaaaag aaaaaaaaaa aaa                   2377
```

MNRSIPVEVDESEPYPSQLLKPIPEYSPEEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH
QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSEPASESVVGALPAEHQFSFMEKRNQWLVSQ
LSAASPDTGHDSDKSDQSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQDVLGIRQLERPL
PLTSVCYPQDLPRPLRSREFPQFEPQRYPACAQMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQ
VIQPALPGQPLPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSFPGLPRHQDQPHHQPPNRAGAPGESLE
CPAELRPQVPQPPSPAAVPRPPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLVNGFQTAID
IFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKQDVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMN
FRFIPVLFPNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGPLPTLQVVPL

Reverse translation of primate, e.g., human, DCRS10 (SEQ ID NO: 24):

atgaaymgnw snathccngt ngargtngay garwsngarc cntayccnws ncarytnytn 60
aarccnathc cngartayws nccngargar garwsngarc cnccngcncc naayathmgn 120
aayatggcnc cnaaywsnyt nwsngcnccn acnatgytnc ayaaywsnws nggngaytty 180
wsncargcnc aywsnacnyt naarytngcn aaycaycarm gnccngtnws nmgncargtn 240
acntgyytnm gnacncargt nytngargay wsngargayw snttytgymg nmgncayccn 300
ggnytnggna argcnttycc nwsnggntgy wsngcngtnw sngarccngc nwsngarwsn 360
gtngtnggng cnytnccngc ngarcaycar ttywsnttya tggaraarmg naaycartgg 420
ytngtnwsnc arytnwsngc ngcnwsnccn gayacnggnc aygaywsnga yaarwsngay 480
carwsnytnc cnaaygcnws ngcngaywsn ytnggnggnw sncargarat ggtncarmgn 540
ccncarccnc aymgnaaymg ngcnggnytn gayytnccna cnathgayac nggntaygay 600
wsncarccnc argaygtnyt nggnathmgn carytngarm gnccnytncc nytnacnwsn 660
gtntgytayc cncargayyt nccnmgnccn ytnmgnwsnm gngarttycc ncarttygar 720
ccncarmgnt ayccngcntg ygcncaratg ytnccnccna ayytnwsncc ncaygcnccn 780
tggaaytayc aytaycaytg yccnggnwsn ccngaycayc argtnccnta yggncaygay 840
tayccnmgng cngcntayca rcargtnath carccngcny tnccnggnca rccnytnccn 900
ggngcnwsng tnmgnggnyt ncayccngtn caraargtna thytnaayta yccnwsnccn 960
tgggaycarg argarmgncc ngcncarmgn gaytgywsnt tyccnggnyt nccnmgncay 1020
cargaycarc cncaycayca rccnccnaay mgngcnggng cnccnggnga rwsnytngar 1080
tgyccngcng arytnmgncc ncargtnccn carccnccnw snccngcngc ngtnccnmgn 1140
ccnccnwsna ayccnccngc nmgnggnacn ytnaaracnw snaayytncc ngargarytn 1200
mgnaargtnt tyathacnta ywsnatggay acngcnatgg argtngtnaa rttygtnaay 1260
ttyytnytng tnaayggntt ycaracngcn athgayatht tygargaymg nathmgnggn 1320
athgayatha thaartggat ggarmgntay ytnmgngaya aracngtnat gathathgtn 1380

```
gcnathwsnc cnaartayaa rcargaygtn garggngcng arwsncaryt ngaygargay 1440
garcayggny tncayacnaa rtayathcay mgnatgatgc arathgartt yathaarcar 1500
ggnwsnatga ayttymgntt yathccngtn ytnttyccna aygcnaaraa rgarcaygtn 1560
ccnacntggy tncaraayac ncaygtntay wsntggccna araayaaraa raayathytn 1620
ytnmgnytny tnmgngarga rgartaygtn gcnccnccnm gnggnccnyt nccnacnytn 1680
cargtngtnc cnytn                                                  1695
```

Rodent, e.g., mouse, embodiment (see SEQ ID NO: 25 and 26).

```
cag gac ctc cct ggg cct ctg agg tcc agg gaa ttg cca cct cag ttt    48
Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe
 1               5                  10                  15

gaa ctt gag agg tat cca atg aac gcc cag ctg ctg ccg ccc cat cct    96
Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro
            20                  25                  30

tcc cca cag gcc cca tgg aac tgt cag tac tac tgc ccc gga ggg ccc   144
Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro
        35                  40                  45

tac cac cac cag gtg cca cac ggc cat ggc tac cct cca gca gca gcc   192
Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
    50                  55                  60

tac cag caa gta ctc cag cct gct ctg cct ggg cag gtc ctt cct ggg   240
Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
65                  70                  75                  80

gca agg gca aga ggc cca cgc cct gtg cag aag gtc atc ctg aat gac   288
Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp
                85                  90                  95

tcc agc ccc caa gac caa gaa gag aga cct gca cag aga gac ttc tct   336
Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser
            100                 105                 110

ttc ccg agg ctc ccg agg gac cag ctc tac cgc cca cca tct aat gga   384
Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly
        115                 120                 125

gtg gaa gcc cct gag gag tcc ttg gac ctt cct gca gag ctg aga cca   432
Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro
    130                 135                 140

cat ggt ccc cag gct cca tcc cta gct gcc gtg cct aga ccc cct agc   480
His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser
145                 150                 155                 160

aac ccc tta gcc cga gga act cta aga acc agc aat ttg cca gaa gaa   528
Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu
                165                 170                 175
```

```
tta cgg aaa gtc ttt atc act tat tct atg gac aca gcc atg gag gtg    576
Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val
                180                 185                 190

gtg aaa ttt gtg aac ttt ctg ttg gtg aac ggc ttc caa act gcg att    624
Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile
            195                 200                 205

gac ata ttt gag gat aga atc cgg ggt att gat atc att aaa tgg atg    672
Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met
    210                 215                 220

gag cgc tat ctt cga gat aag aca gtg atg ata atc gta gca atc agc    720
Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser
225                 230                 235                 240

ccc aaa tac aaa cag gat gtg gaa ggc gct gag tcg cag ctg gac gag    768
Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu
                245                 250                 255

gac gag cat ggc tta cat act aag tac att cat cgg atg atg cag att    816
Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile
            260                 265                 270

gag ttc ata agt cag gga agc atg aac ttc aga ttc atc cct gtg ctc    864
Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu
        275                 280                 285

ttc cca aat gcc aag aag gag cat gtg ccg acc tgg ctt cag aac act    912
Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr
    290                 295                 300

cat gtt tac agc tgg ccc aag aat aag aaa aac atc ctg ctg cgg ctg    960
His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu
305                 310                 315                 320

ctc agg gag gaa gag tat gtg gct cct ccc cga ggc cct ctg ccc acc    1008
Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr
                325                 330                 335

ctt cag gtg gta ccc ttg tgacgatggc cactccagct cagtgccagc          1056
Leu Gln Val Val Pro Leu
            340

ctgttctcac agcattcttc tagcggagct ggctggtggc acccaggccc tggaacacct 1116

cttctacaga gtcctctgtc tcctgagtct gagttgtcct cgctgggctt ccagagcttc 1176

agtgcctgga tgctgcaggt gacagaaaca aacatctatg accacaaaaa ctctcatcac 1236

ttcagctact tttatgagtc ggtcagatgc tctgtgtcct tagaccagtc taaatcatgc 1296

tcaaataata aaatgattat tctttgt                                     1323
```

QDLPGPLRSRELPPQFELERYPMNAQLLPPHPSPQAPWNCQYYCPGGPYHHQVPHGHGYPPAAAYQQVLQPA
LPGQVLPGARARGPRPVQKVILNDSSPQDQEERPAQRDFSFPRLPRDQLYRPPSNGVEAPEESLDLPAELRP
HGPQAPSLAAVPRPPSNPLARGTLRTSNLPEELRKVFITYSMDTAMEVVKFVNFLLVNGFQTAIDIFEDRIR
GIDIIKWMERYLRDKTVMIIVAISPKYKQDVEGAESQLDEDEHGLHTKYIHRMMQIEFISQGSMNFRFIPVL
FPNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGPLPTLQVVPL.

Reverse translation of rodent, e.g., mouse, DCRS6 (SEQ ID NO: 27):

```
cargayytnc cnggnccnyt nmgnwsnmgn garytnccnc cncarttyga rytngarmgn 60
tayccnatga aygcncaryt nytnccnccn cayccnwsnc cncargcncc ntggaaytgy 120
cartaytayt gyccnggngg nccntaycay caycargtnc cncayggnca yggntayccn 180
ccngcngcng cntaycarca rgtnytncar ccngcnytnc cnggncargt nytnccnggn 240
gcnmgngcnm gnggnccnmg nccngtncar aargtnathy tnaaygayws nwsnccncar 300
gaycargarg armgnccngc ncarmgngay ttywsnttyc cnmgnytncc nmgngaycar 360
ytntaymgnc cnccnwsnaa yggngtngar gcnccngarg arwsnytnga yytnccngcn 420
garytnmgnc cncayggncc ncargcnccn wsnytngcng cngtnccnmg nccnccnwsn 480
aayccnytng cnmgnggnac nytnmgnacn wsnaayytnc cngargaryt nmgnaargtn 540
ttyathacnt aywsnatgga yacngcnatg gargtngtna arttygtnaa yttyytnytn 600
gtnaayggnt tycaracngc nathgayath ttygargaym gnathmgngg nathgayath 660
athaartgga tggarmgnta yytnmgngay aaracngtna tgathathgt ngcnathwsn 720
ccnaartaya arcargaygt ngarggngcn garwsncary tngaygarga ygarcayggn 780
ytncayacna artayathca ymgnatgatg carathgart tyathwsnca rggnwsnatg 840
aayttymgnt tyathccngt nytnttyccn aaygcnaara argarcaygt nccnacntgg 900
ytncaraaya cncaygtnta ywsntggccn aaraayaara araayathyt nytnmgnytn 960
ytnmgngarg argartaygt ngcnccnccn mgnggnccny tnccnacnyt ncargtngtn 1020
ccnytn                                                            1026
```

Table 6: Alignment of the cytoplasmic portions of various cytokine receptor subunits. The IL-17R_Hu (SEQ ID NO: 28) is GenBank AAB99730.1(U58917), gi|7657230; the IL-17R_Mu (SEQ ID NO: 29) is GenBank AAC52357.1(U31993), gi|6680411; the IL-17R_Ce (SEQ ID NO: 30) is GenBank AAA811100.1(U39997), gi|1353171; and the DCRS6_Ce (SEQ ID NO: 31) is EMBCAA90543.1(Z50177), gi|7503597. Of particular interest are motifs or features corresponding, in primate DCRS8 to: R/K at 339/340; D/E at 348/349; alpha helical regions from H353-Q365, C370-S381, E389-H396, K410-D414, and D485-H495; beta sheet regions correspond to F400-V404 and F458-Y462; E at 431; E/D at 442/443; Y/F at 458; D/E at 468-470; Y/F at 481; and Q/R/F at 523.

```
DCRS7_Mu     RTALLLHSADG-AGYERLVGALASALSQMP---LRVAVDLWSRRE-LSAHGALAWFHHQR
DCRS7_Hu     RAALLLYSADD-SGFERLVGALASALCQLP---LRVAVDLWSRRE-LSAQGPVAWFHAQR
IL-17R_Hu    RKVWIIYSADH-PLYVDVVLKFAQFLLTACG--TEVALDLLEEQA-ISEAGVMTWVGRQK
IL-17R_Mu    RKVWIVYSADH-PLYVEVVLKFAQFLITACG--TEVALDLLEEQV-ISEVGVMTWVSRQK
DCRS10       RKVFITYSMD----TAMEVVKFVNFLLVNG---FQTAIDIFEDR--IRGIDIIKWMERYL
DCRS10_Mu    RKVFITYSMD----TAMEVVKFVNFLLVNG---FQTAIDIFEDR--IRGIDIIKWMERYL
DCRS9_Hu     RPVLLLHAADS-EAQRRLVGALAELLRAALGGGRDVIVDLWEGRH-VARVGPLPWLWAAR
DCRS8_Hu     PKVFLCYSSKDGQNHMNVVQCFAYFLQDFCG--CEVALDLWEDFS-LCREGQREWVIQKI
IL-17R_Ce    VKVMIVYADDN-DLHTDCVKKLVENLRNCAS--CDPVFDLEKLI--TAEIVPSRWLVDQI
DCRS6_Hu     IKVLVVYPSEI--CFHHTICYFTEFLQNHCR--SEVILEKWQKKK-IAEMGPVQWLATQK
DCRS6_Ce     FKVMLVCPEVS-GRDEDFMMRIADALKKSN---NKVVCDRWFEDSKNAEENMLHWVYEQT
               . :  .           :  : .  *              :            *.

DCRS7_Mu     RRILQEGGVVILLFSPAAVAQCQ---QWLQLQTVEP---GP---HDALAAWLSCVLPDFL
DCRS7_Hu     RQTLQEGGVVVLLFSPGAVALCS---EWLQDGVSGPGAHGP---HDAFRASLSCVLPDFL
IL-17R_Hu    QEMVESNSKIIVLCSRGTRAKWQALLGRGAP-VRLRCDHGKPV-GDLFTAAMNMILPDFK
IL-17R_Mu    QEMVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHWKPA-GDLFTAAMNMILPDFK
DCRS10       R---DKTVMIIVAISPKYKQDVE----GAESQLDED-EHGL---HTKYIHRM-MQIEFIK
DCRS10_Mu    R---DKTVMIIVAISPKYKQDVE----GAESQLDED-EHGL---HTKYIHRM-MQIEFIS
DCRS9_Hu     TRVAREQGTVLLLWSGADLRPVS----GPDP-RAAP-----------LLA----LLHAAP
DCRS8_Hu     H----ESQFIIVVCSKGMKYFVD---KKNYKHKGGGRGSGK---GELFLVAVSAIAEKLR
IL-17R_Ce    S----SLKKFIIVVSDCAEKILD----TEASETHQLVQARP--FADLFGPAMEMIIRDAT
DCRS6_Hu     K----AADKVVFLLSNDVNSVCD----GTCGKSEGSPSENS---QDLFPLAFNLFCSDLR
DCRS6_Ce     K----IAEKIIVFHSAYYHPRCG---IYDVINNFFPCTDPR-----LAHIALT---PEAQ
                       .:.   *

DCRS7_Mu     QGRATGR-----YVGVYFDGLLHPDSVPSPFRVAPLFSLP-SQLPAFLDALQ--GGCSTS
DCRS7_Hu     QGRAPGS-----YVGACFDRLLHPDAVPALFRTVPVFTLP-SQLPDFLGALQ--QPRAPR
IL-17R_Hu    RPACFGT-----YVVCYFSEVSCDGDVPDLFGAAPRYPLM-DRFEEVYFRIQ--DLEMFQ
IL-17R_Mu    RPACFGT-----YVVCYFSGICSERDVPDLFNITSRYPLM-DRFEEVYFRIQ--DLEMFE
DCRS10       QGSMNFR-----FIPVLFPNAK-KEHVPTWLQNTHVYSWP-KNKKNILLRLL-REEEYVA
DCRS10_Mu    QGSMNFR-----FIPVLFPNAK-KEHVPTWLQNTHVYSWP-KNKKNILLRLL-REEEYVA
DCRS9_Hu     RPL---------LLLAYFSRLCAKGDIPPPLRALPRYRLL-RDLPRLLRALD--ARPFAE
DCRS8_Hu     QAKQSSSAALSKFIAVYFDYSC-EGDVPGILDLSTKYRLM-DNLPQLCSHLHSRDHGLQE
IL-17R_Ce    HNFPEAR---KKYAVVRFNYSP---HVPPNLAILNLPTFIPEQFAQLTAFLHN-VEHTER
DCRS6_Hu     SQIHLHK-----YVVVYFREID-TKDDYNALSVCPKYHLM-KDATAFCAELL---HVKQQ
DCRS6_Ce     RSVPKEV----EYVLPRDQKLL--EDAFDITIADPLVIDIPIEDVAIPENVP--IHHESC

DCRS7_Mu     AGRPADRVER-----VT----QALRSALDSCTS-----------
DCRS7_Hu     SGRLQERAEQ-----VS----RALQPALDSYFHPP---------
IL-17R_Hu    PGRMHRVGELSGDNYLRS---PGGRQLRAALDRFRDWQVRCPDW
IL-17R_Mu    PGRMHHVRELTGDNYLQS---PSGRQLKEAVLRFQEWQTQCPDW
DCRS10       P----PRGPL-----------PTLQVVPL---------------
DCRS10_Mu    P----PRGPL-----------PTLQVVPL---------------
DCRS9_Hu     ATSWGRLGAR-----------QRRQSRLELCSR-----------
DCRS8_Hu     PGQHTRQGSR-----RNYFRSKSGRSLYVAICNMHQFIDEEPDW
IL-17R_Ce    ANVTQNISEA------Q------IHEWNLCASRMMSFFVRNPNW
DCRS6_Hu     VS----AGKR-------------SQACHDGCCSL----------
DCRS6_Ce     DSIDSRNNSK-------------THSTDSGVSSLSS----NS--
```

Table 6 shows comparison of the available sequences of primate, rodent, and various other receptors. Various conserved residues are aligned and indicated. The structually homologous cytoplasmic domains most likely signal through pathways like IL-17, e.g., through NFkB. Similar to IL-1 signalling, it is likely that these receptors are invloved in innate immunity and/or development.

As used herein, the term DCRS shall be used to describe a protein comprising amino acid sequences shown in Tables 1-5, respectively. In many cases, a substantial fragment thereof will be functionally or structurally equivalent, including, e.g., an extracellular or intracellular domain. The invention also includes a protein variation of the respective DCRS allele whose sequence is provided, e.g., a mutein or soluble extracellular construct. Typically, such agonists or antagonists will exhibit less than about 10% sequence differences, and thus will often have between 1 and 11 substitutions, e.g., 2-, 3-, 5-, 7-fold, and others. It also encompasses allelic and other variants, e.g., natural polymorphic, of the protein described. Typically, it will bind to its corresponding biological ligand, perhaps in a dimerized state with an alpha receptor subunit, with high affinity, e.g., at least about 100 nM, usually better than about 30 nM, preferably better than about 10 nM, and more preferably at better than about 3 nM. The term shall also be used herein to refer to related naturally occurring forms, e.g., alleles, polymorphic variants, and metabolic variants of the mammalian protein. Preferred forms of the receptor complexes will bind the appropriate ligand with an affinity and selectivity appropriate for a ligand-receptor interaction.

This invention also encompasses combinations of proteins or peptides having substantial amino acid sequence identity with an amino acid sequence in Tables 1-5. It will include sequence variants with relatively few residue substitutions, e.g., preferably less than about 3-5.

A substantial polypeptide "fragment", or "segment", is a stretch of amino acid residues of at least about 8 amino acids, generally at least 10 amino acids, more generally at least 12 amino acids, often at least 14 amino acids, more often at least 16 amino acids, typically at least 18 amino acids, more typically at least 20 amino acids, usually at least 22 amino acids, more usually at least 24 amino acids, preferably at least 26 amino acids, more preferably at least 28 amino acids, and, in particularly preferred embodiments, at least about 30 or more amino acids. This includes, e.g., 40, 50, 60, 70, 85, 100, 115, 130, 150, and other lengths. Sequences of segments of different proteins can be compared to one another over appropriate length stretches, typically between conserved motifs. In many situations, fragments may exhibit functional properties of the intact subunits, e.g., the extracellular domain of the transmembrane receptor may retain the ligand binding features, and may be used to prepare a soluble receptor-like complex.

Amino acid sequence homology, or sequence identity, is determined by optimizing residue matches. In some comparisons, gaps may be introduces, as required. See, e.g., Needleham, et al., (1970) J. Mol. Biol. 48:443-453; Sankoff, et al., (1983) chapter one in Time Warps, String Edits, and Macromolecules: The Theory and Practice of Sequence Comparison, Addison-Wesley, Reading, MA; and software packages from IntelliGenetics, Mountain View, CA; and the University of Wisconsin Genetics Computer Group (GCG), Madison, WI; each of which is incorporated herein by reference. This changes when considering conservative substitutions as matches. Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Homologous amino acid sequences are intended to include natural allelic and interspecies variations in the cytokine sequence. Typical homologous proteins or peptides will have from 50-100% homology (if gaps can be introduced), to 60-100% homology (if conservative substitutions are included) with an amino acid sequence segment of, e.g., Table 3 or 4. Homology measures will be at least about 70%, generally at least 76%, more generally at least 81%, often at least 85%, more often at least 88%, typically at least 90%, more typically at least 92%, usually at least 94%, more usually at least 95%, preferably at least 96%, and more preferably at least 97%, and in particularly preferred embodiments, at least 98% or more. The degree of homology will vary with the length of the compared segments. Homologous proteins or peptides, such as the allelic variants, will share most biological activities with the embodiments described in Tables 1-5.

As used herein, the term "biological activity" is used to describe, without limitation, effects on inflammatory responses, innate immunity, and/or morphogenic development by cytokine-like ligands. For example, these receptors should mediate phosphatase or phosphorylase activities, which activities are easily measured by standard procedures. See, e.g., Hardie, et al. (eds. 1995) The Protein Kinase FactBook vols. I and II, Academic Press, San Diego, CA; Hanks, et al. (1991) Meth. Enzymol. 200:38-62; Hunter, et al. (1992) Cell 70:375-388; Lewin (1990) Cell 61:743-752; Pines, et al. (1991) Cold Spring Harbor Symp. Quant. Biol. 56:449-463; and Parker, et al. (1993) Nature 363:736-738. The receptors, or portions thereof, may be useful as phosphate labeling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognizing antibodies, or antigens capable of binding antibodies.

The terms ligand, agonist, antagonist, and analog of, e.g., a DCRS8 or DCRS9, include molecules that modulate the characteristic cellular responses to cytokine ligand proteins, as well as molecules possessing the more standard structural binding competition features of ligand-receptor interactions, e.g., where the receptor is a natural

receptor or an antibody. The cellular responses likely are typically mediated through receptor tyrosine kinase pathways.

Also, a ligand is a molecule which serves either as a natural ligand to which said receptor, or an analog thereof, binds, or a molecule which is a functional analog of the natural ligand. The functional analog may be a ligand with structural modifications, or may be a wholly unrelated molecule which has a molecular shape which interacts with the appropriate ligand binding determinants. The ligands may serve as agonists or antagonists, see, e.g., Goodman, et al. (eds. 1990) Goodman & Gilman's: The Pharmacological Bases of Therapeutics, Pergamon Press, New York.

Rational drug design may also be based upon structural studies of the molecular shapes of a receptor or antibody and other effectors or ligands. See, e.g., Herz, et al. (1997) J. Recept. Signal Transduct. Res. 17:671-776; and Chaiken, et al. (1996) Trends Biotechnol. 14:369-375. Effectors may be other proteins which mediate other functions in response to ligand binding, or other proteins which normally interact with the receptor. One means for determining which sites interact with specific other proteins is a physical structure determination, e.g., x-ray crystallography or 2 dimensional NMR techniques. These will provide guidance as to which amino acid residues form molecular contact regions. For a detailed description of protein structural determination, see, e.g., Blundell and Johnson (1976) Protein Crystallography, Academic Press, New York, which is hereby incorporated herein by reference.

II. Activities

The cytokine receptor-like proteins will have a number of different biological activities, e.g., modulating cell proliferation, or in phosphate metabolism, being added to or removed from specific substrates, typically proteins. Such will generally result in modulation of an inflammatory function, other innate immunity response, or a morphological effect. The subunit will probably have a specific low affinity binding to the ligand.

The DCRS8 and DCRS9 have characteristic motifs of receptors signaling through the JAK pathway. See, e.g., Ihle, et al. (1997) Stem Cells 15(suppl. 1):105-111; Silvennoinen, et al. (1997) APMIS 105:497-509; Levy (1997) Cytokine Growth Factor Review 8:81-90; Winston and Hunter (1996) Current Biol. 6:668-671; Barrett (1996) Baillieres Clin. Gastroenterol. 10:1-15; and Briscoe, et al. (1996) Philos. Trans. R. Soc. Lond. B. Biol. Sci. 351:167-171.

The biological activities of the cytokine receptor subunits will be related to addition or removal of phosphate moieties to substrates, typically in a specific manner, but occasionally in a non specific manner. Substrates may be identified, or conditions for

enzymatic activity may be assayed by standard methods, e.g., as described in Hardie, et al. (eds. 1995) The Protein Kinase FactBook vols. I and II, Academic Press, San Diego, CA; Hanks, et al. (1991) Meth. Enzymol. 200:38-62; Hunter, et al. (1992) Cell 70:375-388; Lewin (1990) Cell 61:743-752; Pines, et al. (1991) Cold Spring Harbor Symp. Quant. Biol. 56:449-463; and Parker, et al. (1993) Nature 363:736-738.

The receptor subunits may combine to form functional complexes, e.g., which may be useful for binding ligand or preparing antibodies. These will have substantial diagnostic uses, including detection or quantitation.

III. Nucleic Acids

This invention contemplates use of isolated nucleic acid or fragments, e.g., which encode these or closely related proteins, or fragments thereof, e.g., to encode a corresponding polypeptide, preferably one which is biologically active. In addition, this invention covers isolated or recombinant DNAs which encode combinations of such proteins or polypeptides having characteristic sequences, e.g., of the DCRSs. Typically, the nucleic acid is capable of hybridizing, under appropriate conditions, with a nucleic acid sequence segment shown in Tables 1-5, but preferably not with a corresponding segment of other receptors described in Table 6. Said biologically active protein or polypeptide can be a full length protein, or fragment, and will typically have a segment of amino acid sequence highly homologous, e.g., exhibiting significant stretches of identity, to one shown in Tables 1-5. Further, this invention covers the use of isolated or recombinant nucleic acid, or fragments thereof, which encode proteins having fragments which are equivalent to the DCRS8 or DCRS9 proteins. The isolated nucleic acids can have the respective regulatory sequences in the 5' and 3' flanks, e.g., promoters, enhancers, poly-A addition signals, and others from the natural gene. Combinations, as described, are also provided.

An "isolated" nucleic acid is a nucleic acid, e.g., an RNA, DNA, or a mixed polymer, which is substantially pure, e.g., separated from other components which naturally accompany a native sequence, such as ribosomes, polymerases, and flanking genomic sequences from the originating species. The term embraces a nucleic acid sequence which has been removed from its naturally occurring environment, and includes recombinant or cloned DNA isolates, which are thereby distinguishable from naturally occurring compositions, and chemically synthesized analogs or analogs biologically synthesized by heterologous systems. A substantially pure molecule includes isolated forms of the molecule, either completely or substantially pure.

An isolated nucleic acid will generally be a homogeneous composition of molecules, but will, in some embodiments, contain heterogeneity, preferably minor. This

heterogeneity is typically found at the polymer ends or portions not critical to a desired biological function or activity.

A "recombinant" nucleic acid is typically defined either by its method of production or its structure. In reference to its method of production, e.g., a product made by a process, the process is use of recombinant nucleic acid techniques, e.g., involving human intervention in the nucleotide sequence. Typically this intervention involves in vitro manipulation, although under certain circumstances it may involve more classical animal breeding techniques. Alternatively, it can be a nucleic acid made by generating a sequence comprising fusion of two fragments which are not naturally contiguous to each other, but is meant to exclude products of nature, e.g., naturally occurring mutants as found in their natural state. Thus, for example, products made by transforming cells with an unnaturally occurring vector is encompassed, as are nucleic acids comprising sequence derived using any synthetic oligonucleotide process. Such a process is often done to replace a codon with a redundant codon encoding the same or a conservative amino acid, while typically introducing or removing a restriction enzyme sequence recognition site. Alternatively, the process is performed to join together nucleic acid segments of desired functions to generate a single genetic entity comprising a desired combination of functions not found in the commonly available natural forms, e.g., encoding a fusion protein. Restriction enzyme recognition sites are often the target of such artificial manipulations, but other site specific targets, e.g., promoters, DNA replication sites, regulation sequences, control sequences, or other useful features may be incorporated by design. A similar concept is intended for a recombinant, e.g., fusion, polypeptide. This will include a dimeric repeat. Specifically included are synthetic nucleic acids which, by genetic code redundancy, encode equivalent polypeptides to fragments of DCRSs and fusions of sequences from various different related molecules, e.g., other cytokine receptor family members.

A "fragment" in a nucleic acid context is a contiguous segment of at least about 17 nucleotides, generally at least 21 nucleotides, more generally at least 25 nucleotides, ordinarily at least 30 nucleotides, more ordinarily at least 35 nucleotides, often at least 39 nucleotides, more often at least 45 nucleotides, typically at least 50 nucleotides, more typically at least 55 nucleotides, usually at least 60 nucleotides, more usually at least 66 nucleotides, preferably at least 72 nucleotides, more preferably at least 79 nucleotides, and in particularly preferred embodiments will be at least 85 or more nucleotides. Typically, fragments of different genetic sequences can be compared to one another over appropriate length stretches, particularly defined segments such as the domains described below.

A nucleic acid which codes for the DCRS8 or DCRS9 will be particularly useful to identify genes, mRNA, and cDNA species which code for itself or closely related proteins, as well as DNAs which code for polymorphic, allelic, or other genetic variants, e.g., from different individuals or related species. Preferred probes for such screens are those regions of the interleukin which are conserved between different polymorphic variants or which contain nucleotides which lack specificity, and will preferably be full length or nearly so. In other situations, polymorphic variant specific sequences will be more useful.

This invention further covers recombinant nucleic acid molecules and fragments having a nucleic acid sequence identical to or highly homologous to the isolated DNA set forth herein. In particular, the sequences will often be operably linked to DNA segments which control transcription, translation, and DNA replication. These additional segments typically assist in expression of the desired nucleic acid segment.

Homologous, or highly identical, nucleic acid sequences, when compared to one another, e.g., DCRS8 sequences, exhibit significant similarity. The standards for homology in nucleic acids are either measures for homology generally used in the art by sequence comparison or based upon hybridization conditions. Comparative hybridization conditions are described in greater detail below.

Substantial identity in the nucleic acid sequence comparison context means either that the segments, or their complementary strands, when compared, are identical when optimally aligned, with appropriate nucleotide insertions or deletions, in at least about 60% of the nucleotides, generally at least 66%, ordinarily at least 71%, often at least 76%, more often at least 80%, usually at least 84%, more usually at least 88%, typically at least 91%, more typically at least about 93%, preferably at least about 95%, more preferably at least about 96 to 98% or more, and in particular embodiments, as high at about 99% or more of the nucleotides, including, e.g., segments encoding structural domains such as the segments described below. Alternatively, substantial identity will exist when the segments will hybridize under selective hybridization conditions, to a strand or its complement, typically using a sequence derived from Tables 1-5. Typically, selective hybridization will occur when there is at least about 55% homology over a stretch of at least about 14 nucleotides, more typically at least about 65%, preferably at least about 75%, and more preferably at least about 90%. See, Kanehisa (1984) Nucl. Acids Res. 12:203-213, which is incorporated herein by reference. The length of homology comparison, as described, may be over longer stretches, and in certain embodiments will be over a stretch of at least about 17 nucleotides, generally at least about 20 nucleotides, ordinarily at least about 24 nucleotides, usually at least about 28 nucleotides, typically at least about 32 nucleotides, more typically at least about 40 nucleotides, preferably at least

about 50 nucleotides, and more preferably at least about 75 to 100 or more nucleotides. This includes, e.g., 125, 150, 175, 200, 225, 246, 273, and other lengths.

Stringent conditions, in referring to homology in the hybridization context, will be stringent combined conditions of salt, temperature, organic solvents, and other parameters typically controlled in hybridization reactions. Stringent temperature conditions will usually include temperatures in excess of about 30 C, more usually in excess of about 37 C, typically in excess of about 45 C, more typically in excess of about 55 C, preferably in excess of about 65 C, and more preferably in excess of about 70 C. Stringent salt conditions will ordinarily be less than about 500 mM, usually less than about 400 mM, more usually less than about 300 mM, typically less than about 200 mM, preferably less than about 100 mM, and more preferably less than about 80 mM, even down to less than about 20 mM. However, the combination of parameters is much more important than the measure of any single parameter. See, e.g., Wetmur and Davidson (1968) J. Mol. Biol. 31:349-370, which is hereby incorporated herein by reference.

The isolated DNA can be readily modified by nucleotide substitutions, nucleotide deletions, nucleotide insertions, and inversions of nucleotide stretches. These modifications result in novel DNA sequences which encode this protein or its derivatives. These modified sequences can be used to produce mutant proteins (muteins) or to enhance the expression of variant species. Enhanced expression may involve gene amplification, increased transcription, increased translation, and other mechanisms. Such mutant DCRS8–like derivatives include predetermined or site-specific mutations of the protein or its fragments, including silent mutations using genetic code degeneracy. "Mutant DCRS8" as used herein encompasses a polypeptide otherwise falling within the homology definition of the DCRS8 as set forth above, but having an amino acid sequence which differs from that of other cytokine receptor-like proteins as found in nature, whether by way of deletion, substitution, or insertion. In particular, "site specific mutant DCRS8" encompasses a protein having substantial sequence identity with a protein of Table 3, and typically shares most of the biological activities or effects of the forms disclosed herein.

Although site-specific mutation sites are predetermined, mutants need not be site specific. Mammalian DCRS8 mutagenesis can be achieved by making amino acid insertions or deletions in the gene, coupled with expression. Substitutions, deletions, insertions, or many combinations may be generated to arrive at a final construct. Insertions include amino- or carboxy- terminal fusions. Random mutagenesis can be conducted at a target codon and the expressed mammalian DCRS mutants can then be screened for the desired activity, providing some aspect of a structure-activity relationship. Methods for making substitution mutations at predetermined sites in DNA

having a known sequence are well known in the art, e.g., by M13 primer mutagenesis. See also Sambrook, et al. (1989) and Ausubel, et al. (1987 and periodic Supplements).

The mutations in the DNA normally should not place coding sequences out of reading frames and preferably will not create complementary regions that could hybridize to produce secondary mRNA structure such as loops or hairpins.

The phosphoramidite method described by Beaucage and Carruthers (1981) Tetra. Letts. 22:1859-1862, will produce suitable synthetic DNA fragments. A double stranded fragment will often be obtained either by synthesizing the complementary strand and annealing the strand together under appropriate conditions or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

Polymerase chain reaction (PCR) techniques can often be applied in mutagenesis. Alternatively, mutagenesis primers are commonly used methods for generating defined mutations at predetermined sites. See, e.g., Innis, et al. (eds. 1990) PCR Protocols: A Guide to Methods and Applications Academic Press, San Diego, CA; and Dieffenbach and Dveksler (1995; eds.) PCR Primer: A Laboratory Manual Cold Spring Harbor Press, CSH, NY.

Certain embodiments of the invention are directed to combination compositions comprising the receptor or ligand sequences described. In other embodiments, functional portions of the sequences may be joined to encode fusion proteins. In other forms, variants of the described sequences may be substituted.

IV. Proteins, Peptides

As described above, the present invention encompasses primate DCRS6-10, e.g., whose sequences are disclosed in Tables 1-5, and described above. Allelic and other variants are also contemplated, including, e.g., fusion proteins combining portions of such sequences with others, including, e.g., epitope tags and functional domains.

The present invention also provides recombinant proteins, e.g., heterologous fusion proteins using segments from these primate or rodent proteins. A heterologous fusion protein is a fusion of proteins or segments which are naturally not normally fused in the same manner. Thus, the fusion product of, e.g., a DCRS8 with another cytokine receptor is a continuous protein molecule having sequences fused in a typical peptide linkage, typically made as a single translation product and exhibiting properties, e.g., sequence or antigenicity, derived from each source peptide. A similar concept applies to heterologous nucleic acid sequences. Combinations of various designated proteins into complexes are also provided.

In addition, new constructs may be made from combining similar functional or structural domains from other related proteins, e.g., cytokine receptors or Toll-like

receptors, including species variants. For example, ligand-binding or other segments may be "swapped" between different new fusion polypeptides or fragments. See, e.g., Cunningham, et al. (1989) Science 243:1330-1336; and O'Dowd, et al. (1988) J. Biol. Chem. 263:15985-15992, each of which is incorporated herein by reference. Thus, new chimeric polypeptides exhibiting new combinations of specificities will result from the functional linkage of receptor-binding specificities. For example, the ligand binding domains from other related receptor molecules may be added or substituted for other domains of this or related proteins. The resulting protein will often have hybrid function and properties. For example, a fusion protein may include a targeting domain which may serve to provide sequestering of the fusion protein to a particular subcellular organelle.

Candidate fusion partners and sequences can be selected from various sequence data bases, e.g., GenBank, c/o IntelliGenetics, Mountain View, CA; and BCG, University of Wisconsin Biotechnology Computing Group, Madison, WI, which are each incorporated herein by reference. In particular, combinations of polypeptide sequences provided in Tables 1-5 are particularly preferred. Variant forms of the proteins may be substituted in the described combinations.

The present invention particularly provides muteins which bind cytokine-like ligands, and/or which are affected in signal transduction. Structural alignment of human DCRSs with other members of the cytokine receptor family show conserved features/residues. See Table 6. Alignment of the human DCRS8 sequence with other members of the cytokine receptor family indicates various structural and functionally shared features. See also, Bazan, et al. (1996) Nature 379:591; Lodi, et al. (1994) Science 263:1762-1766; Sayle and Milner-White (1995) TIBS 20:374-376; and Gronenberg, et al. (1991) Protein Engineering 4:263-269.

Substitutions with either mouse sequences or human sequences are particularly preferred. Conversely, conservative substitutions away from the ligand binding interaction regions will probably preserve most signaling activities; and conservative substitutions away from the intracellular domains will probably preserve most ligand binding properties.

"Derivatives" of the primate DCRS8 include amino acid sequence mutants, glycosylation variants, metabolic derivatives and covalent or aggregative conjugates with other chemical moieties. Covalent derivatives can be prepared by linkage of functionalities to groups which are found in the DCRS8 amino acid side chains or at the N- or C- termini, e.g., by means which are well known in the art. These derivatives can include, without limitation, aliphatic esters or amides of the carboxyl terminus, or of residues containing carboxyl side chains, O-acyl derivatives of hydroxyl group-containing residues, and N-acyl derivatives of the amino terminal amino acid or amino-group

containing residues, e.g., lysine or arginine. Acyl groups are selected from the group of alkyl-moieties, including C3 to C18 normal alkyl, thereby forming alkanoyl aroyl species.

In particular, glycosylation alterations are included, e.g., made by modifying the glycosylation patterns of a polypeptide during its synthesis and processing, or in further processing steps. Particularly preferred means for accomplishing this are by exposing the polypeptide to glycosylating enzymes derived from cells which normally provide such processing, e.g., mammalian glycosylation enzymes. Deglycosylation enzymes are also contemplated. Also embraced are versions of the same primary amino acid sequence which have other minor modifications, including phosphorylated amino acid residues, e.g., phosphotyrosine, phosphoserine, or phosphothreonine.

A major group of derivatives are covalent conjugates of the receptors or fragments thereof with other proteins of polypeptides. These derivatives can be synthesized in recombinant culture such as N- or C-terminal fusions or by the use of agents known in the art for their usefulness in cross-linking proteins through reactive side groups. Preferred derivatization sites with cross-linking agents are at free amino groups, carbohydrate moieties, and cysteine residues.

Fusion polypeptides between the receptors and other homologous or heterologous proteins are also provided. Homologous polypeptides may be fusions between different receptors, resulting in, for instance, a hybrid protein exhibiting binding specificity for multiple different cytokine ligands, or a receptor which may have broadened or weakened specificity of substrate effect. Likewise, heterologous fusions may be constructed which would exhibit a combination of properties or activities of the derivative proteins. Typical examples are fusions of a reporter polypeptide, e.g., luciferase, with a segment or domain of a receptor, e.g., a ligand-binding segment, so that the presence or location of a desired ligand may be easily determined. See, e.g., Dull, et al., U.S. Patent No. 4,859,609, which is hereby incorporated herein by reference. Other gene fusion partners include glutathione-S-transferase (GST), bacterial ß-galactosidase, trpE, Protein A, ß-lactamase, alpha amylase, alcohol dehydrogenase, and yeast alpha mating factor. See, e.g., Godowski, et al. (1988) Science 241:812-816. Labeled proteins will often be substituted in the described combinations of proteins.

The phosphoramidite method described by Beaucage and Carruthers (1981) Tetra. Letts. 22:1859-1862, will produce suitable synthetic DNA fragments. A double stranded fragment will often be obtained either by synthesizing the complementary strand and annealing the strand together under appropriate conditions or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

Such polypeptides may also have amino acid residues which have been chemically modified by phosphorylation, sulfonation, biotinylation, or the addition or removal of

other moieties, particularly those which have molecular shapes similar to phosphate groups. In some embodiments, the modifications will be useful labeling reagents, or serve as purification targets, e.g., affinity ligands.

Fusion proteins will typically be made by either recombinant nucleic acid methods or by synthetic polypeptide methods. Techniques for nucleic acid manipulation and expression are described generally, for example, in Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed.), Vols. 1-3, Cold Spring Harbor Laboratory, and Ausubel, et al. (eds. 1987 and periodic supplements) Current Protocols in Molecular Biology, Greene/Wiley, New York, which are each incorporated herein by reference. Techniques for synthesis of polypeptides are described, for example, in Merrifield (1963) J. Amer. Chem. Soc. 85:2149-2156; Merrifield (1986) Science 232: 341-347; and Atherton, et al. (1989) Solid Phase Peptide Synthesis: A Practical Approach, IRL Press, Oxford; each of which is incorporated herein by reference. See also Dawson, et al. (1994) Science 266:776-779 for methods to make larger polypeptides.

This invention also contemplates the use of derivatives of a DCRS8 other than variations in amino acid sequence or glycosylation. Such derivatives may involve covalent or aggregative association with chemical moieties. These derivatives generally fall into three classes: (1) salts, (2) side chain and terminal residue covalent modifications, and (3) adsorption complexes, for example with cell membranes. Such covalent or aggregative derivatives are useful as immunogens, as reagents in immunoassays, or in purification methods such as for affinity purification of a receptor or other binding molecule, e.g., an antibody. For example, a cytokine ligand can be immobilized by covalent bonding to a solid support such as cyanogen bromide-activated Sepharose, by methods which are well known in the art, or adsorbed onto polyolefin surfaces, with or without glutaraldehyde cross-linking, for use in the assay or purification of a cytokine receptor, antibodies, or other similar molecules. The ligand can also be labeled with a detectable group, for example radioiodinated by the chloramine T procedure, covalently bound to rare earth chelates, or conjugated to another fluorescent moiety for use in diagnostic assays.

A combination, e.g., including a DCRS8, of this invention can be used as an immunogen for the production of antisera or antibodies specific, e.g., capable of distinguishing between other cytokine receptor family members, for the combinations described. The complexes can be used to screen monoclonal antibodies or antigen-binding fragments prepared by immunization with various forms of impure preparations containing the protein. In particular, the term "antibodies" also encompasses antigen binding fragments of natural antibodies, e.g., Fab, Fab2, Fv, etc. The purified DCRS8 can also be used as a reagent to detect antibodies generated in response to the presence of

elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. Additionally, DCRS8 fragments may also serve as immunogens to produce the antibodies of the present invention, as described immediately below. For example, this invention contemplates antibodies having binding affinity to or being raised against the amino acid sequences shown in Tables 1-5, fragments thereof, or various homologous peptides. In particular, this invention contemplates antibodies having binding affinity to, or having been raised against, specific fragments which are predicted to be, or actually are, exposed at the exterior protein surface of the native DCRS8 or DCRS9. Complexes of combinations of proteins will also be useful, and antibody preparations thereto can be made.

The blocking of physiological response to the receptor ligands may result from the inhibition of binding of the ligand to the receptor, likely through competitive inhibition. Thus, in vitro assays of the present invention will often use antibodies or antigen binding segments of these antibodies, or fragments attached to solid phase substrates. These assays will also allow for the diagnostic determination of the effects of either ligand binding region mutations and modifications, or other mutations and modifications, e.g., which affect signaling or enzymatic function.

This invention also contemplates the use of competitive drug screening assays, e.g., where neutralizing antibodies to the receptor complexes or fragments compete with a test compound for binding to a ligand or other antibody. In this manner, the neutralizing antibodies or fragments can be used to detect the presence of a polypeptide which shares one or more binding sites to a receptor and can also be used to occupy binding sites on a receptor that might otherwise bind a ligand.

V. Making Nucleic Acids and Protein

DNA which encodes the protein or fragments thereof can be obtained by chemical synthesis, screening cDNA libraries, or by screening genomic libraries prepared from a wide variety of cell lines or tissue samples. Natural sequences can be isolated using standard methods and the sequences provided herein, e.g., in Tables 1-5. Other species counterparts can be identified by hybridization techniques, or by various PCR techniques, combined with or by searching in sequence databases, e.g., GenBank.

This DNA can be expressed in a wide variety of host cells for the synthesis of a full-length receptor or fragments which can in turn, for example, be used to generate polyclonal or monoclonal antibodies; for binding studies; for construction and expression of modified ligand binding or kinase/phosphatase domains; and for structure/function studies. Variants or fragments can be expressed in host cells that are transformed or transfected with appropriate expression vectors. These molecules can be substantially

free of protein or cellular contaminants, other than those derived from the recombinant host, and therefore are particularly useful in pharmaceutical compositions when combined with a pharmaceutically acceptable carrier and/or diluent. The protein, or portions thereof, may be expressed as fusions with other proteins. Combinations of the described proteins, or nucleic acids encoding them, are particularly interesting.

Expression vectors are typically self-replicating DNA or RNA constructs containing the desired receptor gene or its fragments, usually operably linked to suitable genetic control elements that are recognized in a suitable host cell. These control elements are capable of effecting expression within a suitable host. The multiple genes may be coordinately expressed, and may be on a polycistronic message. The specific type of control elements necessary to effect expression will depend upon the eventual host cell used. Generally, the genetic control elements can include a prokaryotic promoter system or a eukaryotic promoter expression control system, and typically include a transcriptional promoter, an optional operator to control the onset of transcription, transcription enhancers to elevate the level of mRNA expression, a sequence that encodes a suitable ribosome binding site, and sequences that terminate transcription and translation. Expression vectors also usually contain an origin of replication that allows the vector to replicate independently of the host cell.

The vectors of this invention include those which contain DNA which encodes a combination of proteins, as described, or a biologically active equivalent polypeptide. The DNA can be under the control of a viral promoter and can encode a selection marker. This invention further contemplates use of such expression vectors which are capable of expressing eukaryotic cDNAs coding for such proteins in a prokaryotic or eukaryotic host, where the vector is compatible with the host and where the eukaryotic cDNAs are inserted into the vector such that growth of the host containing the vector expresses the cDNAs in question. Usually, expression vectors are designed for stable replication in their host cells or for amplification to greatly increase the total number of copies of the desirable gene per cell. It is not always necessary to require that an expression vector replicate in a host cell, e.g., it is possible to effect transient expression of the protein or its fragments in various hosts using vectors that do not contain a replication origin that is recognized by the host cell. It is also possible to use vectors that cause integration of the protein encoding portions into the host DNA by recombination.

Vectors, as used herein, comprise plasmids, viruses, bacteriophage, integratable DNA fragments, and other vehicles which enable the integration of DNA fragments into the genome of the host. Expression vectors are specialized vectors which contain genetic control elements that effect expression of operably linked genes. Plasmids are the most commonly used form of vector but all other forms of vectors which serve an equivalent

function and which are, or become, known in the art are suitable for use herein. See, e.g., Pouwels, et al. (1985 and Supplements) Cloning Vectors: A Laboratory Manual, Elsevier, N.Y., and Rodriguez, et al. (eds. 1988) Vectors: A Survey of Molecular Cloning Vectors and Their Uses, Buttersworth, Boston, which are incorporated herein by reference.

Transformed cells are cells, preferably mammalian, that have been transformed or transfected with vectors constructed using recombinant DNA techniques. Transformed host cells usually express the desired proteins, but for purposes of cloning, amplifying, and manipulating its DNA, do not need to express the subject proteins. This invention further contemplates culturing transformed cells in a nutrient medium, thus permitting the proteins to accumulate. The proteins can be recovered, either from the culture or, in certain instances, from the culture medium.

For purposes of this invention, nucleic sequences are operably linked when they are functionally related to each other. For example, DNA for a presequence or secretory leader is operably linked to a polypeptide if it is expressed as a preprotein or participates in directing the polypeptide to the cell membrane or in secretion of the polypeptide. A promoter is operably linked to a coding sequence if it controls the transcription of the polypeptide; a ribosome binding site is operably linked to a coding sequence if it is positioned to permit translation. Usually, operably linked means contiguous and in reading frame, however, certain genetic elements such as repressor genes are not contiguously linked but still bind to operator sequences that in turn control expression.

Suitable host cells include prokaryotes, lower eukaryotes, and higher eukaryotes. Prokaryotes include both gram negative and gram positive organisms, e.g., E. coli and B. subtilis. Lower eukaryotes include yeasts, e.g., S. cerevisiae and Pichia, and species of the genus Dictyostelium. Higher eukaryotes include established tissue culture cell lines from animal cells, both of non-mammalian origin, e.g., insect cells, and birds, and of mammalian origin, e.g., human, primates, and rodents.

Prokaryotic host-vector systems include a wide variety of vectors for many different species. As used herein, E. coli and its vectors will be used generically to include equivalent vectors used in other prokaryotes. A representative vector for amplifying DNA is pBR322 or many of its derivatives. Vectors that can be used to express the receptor or its fragments include, but are not limited to, such vectors as those containing the lac promoter (pUC-series); trp promoter (pBR322-trp); Ipp promoter (the pIN-series); lambda-pP or pR promoters (pOTS); or hybrid promoters such as ptac (pDR540). See Brosius, et al. (1988) "Expression Vectors Employing Lambda-, trp-, lac-, and Ipp-derived Promoters", in Vectors: A Survey of Molecular Cloning Vectors and Their Uses, (eds. Rodriguez and Denhardt), Buttersworth, Boston, Chapter 10, pp. 205-236, which is incorporated herein by reference.

Lower eukaryotes, e.g., yeasts and Dictyostelium, may be transformed with DCRS8 sequence containing vectors. For purposes of this invention, the most common lower eukaryotic host is the baker's yeast, Saccharomyces cerevisiae. It will be used to generically represent lower eukaryotes although a number of other strains and species are also available. Yeast vectors typically consist of a replication origin (unless of the integrating type), a selection gene, a promoter, DNA encoding the receptor or its fragments, and sequences for translation termination, polyadenylation, and transcription termination. Suitable expression vectors for yeast include such constitutive promoters as 3-phosphoglycerate kinase and various other glycolytic enzyme gene promoters or such inducible promoters as the alcohol dehydrogenase 2 promoter or metallothionine promoter. Suitable vectors include derivatives of the following types: self-replicating low copy number (such as the YRp-series), self-replicating high copy number (such as the YEp-series); integrating types (such as the YIp-series), or mini-chromosomes (such as the YCp-series).

Higher eukaryotic tissue culture cells are normally the preferred host cells for expression of the functionally active interleukin or receptor proteins. In principle, many higher eukaryotic tissue culture cell lines are workable, e.g., insect baculovirus expression systems, whether from an invertebrate or vertebrate source. However, mammalian cells are preferred. Transformation or transfection and propagation of such cells has become a routine procedure. Examples of useful cell lines include HeLa cells, Chinese hamster ovary (CHO) cell lines, baby rat kidney (BRK) cell lines, insect cell lines, bird cell lines, and monkey (COS) cell lines. Expression vectors for such cell lines usually include an origin of replication, a promoter, a translation initiation site, RNA splice sites (if genomic DNA is used), a polyadenylation site, and a transcription termination site. These vectors also usually contain a selection gene or amplification gene. Suitable expression vectors may be plasmids, viruses, or retroviruses carrying promoters derived, e.g., from such sources as from adenovirus, SV40, parvoviruses, vaccinia virus, or cytomegalovirus. Representative examples of suitable expression vectors include pCDNA1; pCD, see Okayama, et al. (1985) Mol. Cell Biol. 5:1136-1142; pMC1neo PolyA, see Thomas, et al. (1987) Cell 51:503-512; and a baculovirus vector such as pAC 373 or pAC 610.

For secreted proteins and some membrane proteins, an open reading frame usually encodes a polypeptide that consists of a mature or secreted product covalently linked at its N-terminus to a signal peptide. The signal peptide is cleaved prior to secretion of the mature, or active, polypeptide. The cleavage site can be predicted with a high degree of accuracy from empirical rules, e.g., von-Heijne (1986) Nucleic Acids Research 14:4683-4690; and Nielsen, et al. (1997) Protein Eng. 10:1-12, and the precise amino acid composition of the signal peptide often does not appear to be critical to its function, e.g.,

Randall, et al. (1989) Science 243:1156-1159; and Kaiser, et al. (1987) Science 235:312-317. The mature proteins of the invention can be readily determined using standard methods.

It will often be desired to express these polypeptides in a system which provides a specific or defined glycosylation pattern. In this case, the usual pattern will be that provided naturally by the expression system. However, the pattern will be modifiable by exposing the polypeptide, e.g., an unglycosylated form, to appropriate glycosylating proteins introduced into a heterologous expression system. For example, the receptor gene may be co-transformed with one or more genes encoding mammalian or other glycosylating enzymes. Using this approach, certain mammalian glycosylation patterns will be achievable in prokaryote or other cells. Expression in prokaryote cells will typically lead to unglycosylated forms of protein.

The source of DCRS8 can be a eukaryotic or prokaryotic host expressing recombinant DCRS8, such as is described above. The source can also be a cell line, but other mammalian cell lines are also contemplated by this invention, with the preferred cell line being from the human species.

Now that the sequences are known, the primate DCRS8 or DCRS9, fragments, or derivatives thereof can be prepared by conventional processes for synthesizing peptides. These include processes such as are described in Stewart and Young (1984) Solid Phase Peptide Synthesis, Pierce Chemical Co., Rockford, IL; Bodanszky and Bodanszky (1984) The Practice of Peptide Synthesis, Springer-Verlag, New York; and Bodanszky (1984) The Principles of Peptide Synthesis, Springer-Verlag, New York; all of each which are incorporated herein by reference. For example, an azide process, an acid chloride process, an acid anhydride process, a mixed anhydride process, an active ester process (for example, p-nitrophenyl ester, N-hydroxysuccinimide ester, or cyanomethyl ester), a carbodiimidazole process, an oxidative-reductive process, or a dicyclohexylcarbodiimide (DCCD)/additive process can be used. Solid phase and solution phase syntheses are both applicable to the foregoing processes. Similar techniques can be used with partial DCRS8 or DCRS9 sequences.

The DCRS8 proteins, fragments, or derivatives are suitably prepared in accordance with the above processes as typically employed in peptide synthesis, generally either by a so-called stepwise process which comprises condensing an amino acid to the terminal amino acid, one by one in sequence, or by coupling peptide fragments to the terminal amino acid. Amino groups that are not being used in the coupling reaction typically must be protected to prevent coupling at an incorrect location.

If a solid phase synthesis is adopted, the C-terminal amino acid is bound to an insoluble carrier or support through its carboxyl group. The insoluble carrier is not

particularly limited as long as it has a binding capability to a reactive carboxyl group. Examples of such insoluble carriers include halomethyl resins, such as chloromethyl resin or bromomethyl resin, hydroxymethyl resins, phenol resins, tert-alkyloxycarbonylhydrazidated resins, and the like.

An amino group-protected amino acid is bound in sequence through condensation of its activated carboxyl group and the reactive amino group of the previously formed peptide or chain, to synthesize the peptide step by step. After synthesizing the complete sequence, the peptide is split off from the insoluble carrier to produce the peptide. This solid-phase approach is generally described by Merrifield, et al. (1963) in J. Am. Chem. Soc. 85:2149-2156, which is incorporated herein by reference.

The prepared protein and fragments thereof can be isolated and purified from the reaction mixture by means of peptide separation, e.g., by extraction, precipitation, electrophoresis, various forms of chromatography, and the like. The receptors of this invention can be obtained in varying degrees of purity depending upon desired uses. Purification can be accomplished by use of the protein purification techniques disclosed herein, see below, or by the use of the antibodies herein described in methods of immunoabsorbant affinity chromatography. This immunoabsorbant affinity chromatography is carried out by first linking the antibodies to a solid support and then contacting the linked antibodies with solubilized lysates of appropriate cells, lysates of other cells expressing the receptor, or lysates or supernatants of cells producing the protein as a result of DNA techniques, see below.

Generally, the purified protein will be at least about 40% pure, ordinarily at least about 50% pure, usually at least about 60% pure, typically at least about 70% pure, more typically at least about 80% pure, preferable at least about 90% pure and more preferably at least about 95% pure, and in particular embodiments, 97%-99% or more. Purity will usually be on a weight basis, but can also be on a molar basis. Different assays will be applied as appropriate. Individual proteins may be purified and thereafter combined.

VI. Antibodies

Antibodies can be raised to the various mammalian, e.g., primate DCRS8 or DCRS9 proteins and fragments thereof, both in naturally occurring native forms and in their recombinant forms, the difference being that antibodies to the active receptor are more likely to recognize epitopes which are only present in the native conformations. Denatured antigen detection can also be useful in, e.g., Western analysis. Anti-idiotypic antibodies are also contemplated, which would be useful as agonists or antagonists of a natural receptor or an antibody.

Antibodies, including binding fragments and single chain versions, against predetermined fragments of the protein can be raised by immunization of animals with conjugates of the fragments with immunogenic proteins. Monoclonal antibodies are prepared from cells secreting the desired antibody. These antibodies can be screened for binding to normal or defective protein, or screened for agonistic or antagonistic activity. These monoclonal antibodies will usually bind with at least a K_D of about 1 mM, more usually at least about 300 μM, typically at least about 100μM, more typically at least about 30 μM, preferably at least about 10 μM, and more preferably at least about 3 μM or better.

The antibodies, including antigen binding fragments, of this invention can have significant diagnostic or therapeutic value. They can be potent antagonists that bind to the receptor and inhibit binding to ligand or inhibit the ability of the receptor to elicit a biological response, e.g., act on its substrate. They also can be useful as non-neutralizing antibodies and can be coupled to toxins or radionuclides to bind producing cells, or cells localized to the source of the interleukin. Further, these antibodies can be conjugated to drugs or other therapeutic agents, either directly or indirectly by means of a linker.

The antibodies of this invention can also be useful in diagnostic applications. As capture or non-neutralizing antibodies, they might bind to the receptor without inhibiting ligand or substrate binding. As neutralizing antibodies, they can be useful in competitive binding assays. They will also be useful in detecting or quantifying ligand. They may be used as reagents for Western blot analysis, or for immunoprecipitation or immunopurification of the respective protein. Likewise, nucleic acids and proteins may be immobilized to solid substrates for affinity purification or detection methods. The substrates may be, e.g., solid resin beads or sheets of plastic.

Protein fragments may be joined to other materials, particularly polypeptides, as fused or covalently joined polypeptides to be used as immunogens. Mammalian cytokine receptors and fragments may be fused or covalently linked to a variety of immunogens, such as keyhole limpet hemocyanin, bovine serum albumin, tetanus toxoid, etc. See (1969) Microbiology, Hoeber Medical Division, Harper and Row; Landsteiner (1962) Specificity of Serological Reactions, Dover Publications, New York; and Williams, et al. (1967) Methods in Immunology and Immunochemistry, Vol. 1, Academic Press, New York; each of which is incorporated herein by reference, for descriptions of methods of preparing polyclonal antisera. A typical method involves hyperimmunization of an animal with an antigen. The blood of the animal is then collected shortly after the repeated immunizations and the gamma globulin is isolated.

In some instances, it is desirable to prepare monoclonal antibodies from various mammalian hosts, such as mice, rodents, primates, humans, etc. Description of

techniques for preparing such monoclonal antibodies may be found in, e.g., Stites, et al. (eds.) Basic and Clinical Immunology (4th ed.), Lange Medical Publications, Los Altos, CA, and references cited therein; Harlow and Lane (1988) Antibodies: A Laboratory Manual, CSH Press; Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press, New York; and particularly in Kohler and Milstein (1975) Nature 256:495-497, which discusses one method of generating monoclonal antibodies. Each of these references is incorporated herein by reference. Summarized briefly, this method involves injecting an animal with an immunogen. The animal is then sacrificed and cells taken from its spleen, which are then fused with myeloma cells. The result is a hybrid cell or "hybridoma" that is capable of reproducing in vitro. The population of hybridomas is then screened to isolate individual clones, each of which secrete a single antibody species to the immunogen. In this manner, the individual antibody species obtained are the products of immortalized and cloned single B cells from the immune animal generated in response to a specific site recognized on the immunogenic substance.

Other suitable techniques involve in vitro exposure of lymphocytes to the antigenic polypeptides or alternatively to selection of libraries of antibodies in phage or similar vectors. See, Huse, et al. (1989) "Generation of a Large Combinatorial Library of the Immunoglobulin Repertoire in Phage Lambda," Science 246:1275-1281; and Ward, et al. (1989) Nature 341:544-546, each of which is incorporated herein by reference. The polypeptides and antibodies of the present invention may be used with or without modification, including chimeric or humanized antibodies. Frequently, the polypeptides and antibodies will be labeled by joining, either covalently or non-covalently, a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, chemiluminescent moieties, magnetic particles, and the like. Patents, teaching the use of such labels include U.S. Patent Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241. Also, recombinant or chimeric immunoglobulins may be produced, see Cabilly, U.S. Patent No. 4,816,567; or made in transgenic mice, see Mendez, et al. (1997) Nature Genetics 15:146-156; Abgenix; and Medarex. These references are incorporated herein by reference.

The antibodies of this invention can also be used for affinity chromatography in isolating the DCRS8 proteins or peptides. Columns can be prepared where the antibodies are linked to a solid support, e.g., particles, such as agarose, Sephadex, or the like, where a cell lysate may be passed through the column, the column washed, followed by increasing concentrations of a mild denaturant, whereby the purified protein will be

released. Alternatively, the protein may be used to purify antibody. Appropriate cross absorptions or depletions may be applied.

The antibodies may also be used to screen expression libraries for particular expression products. Usually the antibodies used in such a procedure will be labeled with a moiety allowing easy detection of presence of antigen by antibody binding.

Antibodies raised against a cytokine receptor will also be used to raise anti-idiotypic antibodies. These will be useful in detecting or diagnosing various immunological conditions related to expression of the protein or cells which express the protein. They also will be useful as agonists or antagonists of the ligand, which may be competitive inhibitors or substitutes for naturally occurring ligands.

A cytokine receptor protein that specifically binds to or that is specifically immunoreactive with an antibody generated against a defined immunogen, such as an immunogen consisting of the amino acid sequence of SEQ ID NO: 14, is typically determined in an immunoassay. The immunoassay typically uses a polyclonal antiserum which was raised, e.g., to a protein of SEQ ID NO: 14. This antiserum is selected to have low crossreactivity against other cytokine receptor family members, preferably from the same species, and any such crossreactivity is removed by immunoabsorption prior to use in the immunoassay.

In order to produce antisera for use in an immunoassay, the protein, e.g., of SEQ ID NO: 14, is isolated as described herein. For example, recombinant protein may be produced in a mammalian cell line. An appropriate host, e.g., an inbred strain of mice such as Balb/c, is immunized with the selected protein, typically using a standard adjuvant, such as Freund's adjuvant, and a standard mouse immunization protocol (see Harlow and Lane, supra). Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Polyclonal sera are collected and titered against the immunogen protein in an immunoassay, e.g., a solid phase immunoassay with the immunogen immobilized on a solid support. Polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against other cytokine receptor family members using a competitive binding immunoassay such as the one described in Harlow and Lane, supra, at pages 570-573. Preferably at least two cytokine receptor family members are used in this determination. These cytokine receptor family members can be produced as recombinant proteins and isolated using standard molecular biology and protein chemistry techniques as described herein.

Immunoassays in the competitive binding format can be used for the crossreactivity determinations. For example, the protein of SEQ ID NO: 14 can be immobilized to a solid support. Proteins added to the assay compete with the binding of

the antisera to the immobilized antigen. The ability of the above proteins to compete with the binding of the antisera to the immobilized protein is compared to the other proteins. The percent crossreactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% crossreactivity with each of the proteins listed above are selected and pooled. The cross-reacting antibodies are then removed from the pooled antisera by immunoabsorption with the above-listed proteins.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein to the immunogen protein (e.g., the DCRS8 like protein of SEQ ID NO: 14). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required is less than twice the amount of the protein of the selected protein or proteins that is required, then the second protein is said to specifically bind to an antibody generated to the immunogen.

It is understood that these cytokine receptor proteins are members of a family of homologous proteins that comprise at least 9 so far identified members, 6 mammalian and 3 worm embodiments. For a particular gene product, such as the DCRS8, the term refers not only to the amino acid sequences disclosed herein, but also to other proteins that are allelic, non-allelic, or species variants. It is also understood that the terms include nonnatural mutations introduced by deliberate mutation using conventional recombinant technology such as single site mutation, or by excising short sections of DNA encoding the respective proteins, or by substituting new amino acids, or adding new amino acids. Such minor alterations typically will substantially maintain the immunoidentity of the original molecule and/or its biological activity. Thus, these alterations include proteins that are specifically immunoreactive with a designated naturally occurring DCRS8 protein. The biological properties of the altered proteins can be determined by expressing the protein in an appropriate cell line and measuring the appropriate effect, e.g., upon transfected lymphocytes. Particular protein modifications considered minor would include conservative substitution of amino acids with similar chemical properties, as described above for the cytokine receptor family as a whole. By aligning a protein optimally with the protein of the cytokine receptors and by using the conventional immunoassays described herein to determine immunoidentity, one can determine the protein compositions of the invention.

VII. Kits and quantitation

Both naturally occurring and recombinant forms of the cytokine receptor like molecules of this invention are particularly useful in kits and assay methods. For

example, these methods would also be applied to screening for binding activity, e.g., ligands for these proteins. Several methods of automating assays have been developed in recent years so as to permit screening of tens of thousands of compounds per year. See, e.g., a BIOMEK automated workstation, Beckman Instruments, Palo Alto, California, and Fodor, et al. (1991) Science 251:767-773, which is incorporated herein by reference. The latter describes means for testing binding by a plurality of defined polymers synthesized on a solid substrate. The development of suitable assays to screen for a ligand or agonist/antagonist homologous proteins can be greatly facilitated by the availability of large amounts of purified, soluble cytokine receptors in an active state such as is provided by this invention.

Purified protein can be coated directly onto plates for use in the aforementioned ligand screening techniques. However, non-neutralizing antibodies to these proteins can be used as capture antibodies to immobilize the respective receptor on the solid phase, useful, e.g., in diagnostic uses.

This invention also contemplates use of receptor subunit, fragments thereof, peptides, and their fusion products in a variety of diagnostic kits and methods for detecting the presence of the protein or its ligand. Alternatively, or additionally, antibodies against the molecules may be incorporated into the kits and methods. Typically the kit will have a compartment containing, e.g., a DCRS8 peptide or gene segment or a reagent which recognizes one or the other. Typically, recognition reagents, in the case of peptide, would be a receptor or antibody, or in the case of a gene segment, would usually be a hybridization probe.

A preferred kit for determining the concentration of DCRS8 in a sample would typically comprise a labeled compound, e.g., ligand or antibody, having known binding affinity for DCRS8, a source of DCRS8 (naturally occurring or recombinant) as a positive control, and a means for separating the bound from free labeled compound, e.g., a solid phase for immobilizing the DCRS8 in the test sample. Compartments containing reagents, and instructions, will normally be provided. Appropriate nucleic acid or protein containing kits are also provided.

Antibodies, including antigen binding fragments, specific for mammalian DCRS8 or a peptide fragment, or receptor fragments are useful in diagnostic applications to detect the presence of elevated levels of ligand and/or its fragments. Diagnostic assays may be homogeneous (without a separation step between free reagent and antibody-antigen complex) or heterogeneous (with a separation step). Various commercial assays exist, such as radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), enzyme immunoassay (EIA), enzyme-multiplied immunoassay technique (EMIT), substrate-labeled fluorescent immunoassay (SLFIA) and the like. For example, unlabeled

antibodies can be employed by using a second antibody which is labeled and which recognizes the antibody to a cytokine receptor or to a particular fragment thereof. These assays have also been extensively discussed in the literature. See, e.g., Harlow and Lane (1988) Antibodies: A Laboratory Manual, CSH, and Coligan (ed. 1991 and periodic supplements) Current Protocols In Immunology Greene/Wiley, New York.

Anti-idiotypic antibodies may have similar use to serve as agonists or antagonists of cytokine receptors. These should be useful as therapeutic reagents under appropriate circumstances.

Frequently, the reagents for diagnostic assays are supplied in kits, so as to optimize the sensitivity of the assay. For the subject invention, depending upon the nature of the assay, the protocol, and the label, either labeled or unlabeled antibody, or labeled ligand is provided. This is usually in conjunction with other additives, such as buffers, stabilizers, materials necessary for signal production such as substrates for enzymes, and the like. Preferably, the kit will also contain instructions for proper use and disposal of the contents after use. Typically the kit has compartments for each useful reagent, and will contain instructions for proper use and disposal of reagents. Desirably, the reagents are provided as a dry lyophilized powder, where the reagents may be reconstituted in an aqueous medium having appropriate concentrations for performing the assay.

The aforementioned constituents of the diagnostic assays may be used without modification or may be modified in a variety of ways. For example, labeling may be achieved by covalently or non-covalently joining a moiety which directly or indirectly provides a detectable signal. In many of these assays, a test compound, cytokine receptor, or antibodies thereto can be labeled either directly or indirectly. Possibilities for direct labeling include label groups: radiolabels such as ^{125}I, enzymes (U.S. Pat. No. 3,645,090) such as peroxidase and alkaline phosphatase, and fluorescent labels (U.S. Pat. No. 3,940,475) capable of monitoring the change in fluorescence intensity, wavelength shift, or fluorescence polarization. Both of the patents are incorporated herein by reference. Possibilities for indirect labeling include biotinylation of one constituent followed by binding to avidin coupled to one of the above label groups.

There are also numerous methods of separating the bound from the free ligand, or alternatively the bound from the free test compound. The cytokine receptor can be immobilized on various matrixes followed by washing. Suitable matrices include plastic such as an ELISA plate, filters, and beads. Methods of immobilizing the receptor to a matrix include, without limitation, direct adhesion to plastic, use of a capture antibody, chemical coupling, and biotin-avidin. The last step in this approach involves the precipitation of antibody/antigen complex by any of several methods including those

utilizing, e.g., an organic solvent such as polyethylene glycol or a salt such as ammonium sulfate. Other suitable separation techniques include, without limitation, the fluorescein antibody magnetizable particle method described in Rattle, et al. (1984) Clin. Chem. 30(9):1457-1461, and the double antibody magnetic particle separation as described in U.S. Pat. No. 4,659,678, each of which is incorporated herein by reference.

The methods for linking protein or fragments to various labels have been extensively reported in the literature and do not require detailed discussion here. Many of the techniques involve the use of activated carboxyl groups either through the use of carbodiimide or active esters to form peptide bonds, the formation of thioethers by reaction of a mercapto group with an activated halogen such as chloroacetyl, or an activated olefin such as maleimide, for linkage, or the like. Fusion proteins will also find use in these applications.

Another diagnostic aspect of this invention involves use of oligonucleotide or polynucleotide sequences taken from the sequence of an cytokine receptor. These sequences can be used as probes for detecting levels of the respective cytokine receptor in patients suspected of having an immunological disorder. The preparation of both RNA and DNA nucleotide sequences, the labeling of the sequences, and the preferred size of the sequences has received ample description and discussion in the literature. Normally an oligonucleotide probe should have at least about 14 nucleotides, usually at least about 18 nucleotides, and the polynucleotide probes may be up to several kilobases. Various labels may be employed, most commonly radionuclides, particularly ^{32}P. However, other techniques may also be employed, such as using biotin modified nucleotides for introduction into a polynucleotide. The biotin then serves as the site for binding to avidin or antibodies, which may be labeled with a wide variety of labels, such as radionuclides, fluorescers, enzymes, or the like. Alternatively, antibodies may be employed which can recognize specific duplexes, including DNA duplexes, RNA duplexes, DNA-RNA hybrid duplexes, or DNA-protein duplexes. The antibodies in turn may be labeled and the assay carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected. The use of probes to the novel RNA may be carried out in conventional techniques such as nucleic acid hybridization, plus and minus screening, recombinational probing, hybrid released translation (HRT), and hybrid arrested translation (HART). Antisense nucleic acids, which may be used to block protein expression, are also provided. See, e.g., Isis Pharmaceuticals, Sequitur, Inc., or Hybridon. This also includes amplification techniques such as polymerase chain reaction (PCR).

Diagnostic kits which also test for the qualitative or quantitative presence of other markers are also contemplated. Diagnosis or prognosis may depend on the combination

of multiple indications used as markers. Thus, kits may test for combinations of markers. See, e.g., Viallet, et al. (1989) Progress in Growth Factor Res. 1:89-97.

VIII. Therapeutic Utility

This invention provides reagents with significant therapeutic value. See, e.g., Levitzki (1996) Curr. Opin. Cell Biol. 8:239-244. The cytokine receptors (naturally occurring or recombinant), fragments thereof, mutein receptors, and antibodies, along with compounds identified as having binding affinity to the receptors or antibodies, should be useful in the treatment of conditions exhibiting abnormal expression of the receptors of their ligands. Such abnormality will typically be manifested by immunological disorders, e.g., innate immunity, or developmentally. Additionally, this invention should provide therapeutic value in various diseases or disorders associated with abnormal expression or abnormal triggering of response to the ligand. For example, the IL-1 ligands have been suggested to be involved in morphologic development, e.g., dorso-ventral polarity determination, and immune responses, particularly the primitive innate responses. See, e.g., Sun, et al. (1991) Eur. J. Biochem. 196:247-254; and Hultmark (1994) Nature 367:116-117.

Recombinant cytokine receptors, muteins, agonist or antagonist antibodies thereto, or antibodies can be purified and then administered to a patient. These reagents can be combined for therapeutic use with additional active ingredients, e.g., in conventional pharmaceutically acceptable carriers or diluents, along with physiologically innocuous stabilizers and excipients. These combinations can be sterile, e.g., filtered, and placed into dosage forms as by lyophilization in dosage vials or storage in stabilized aqueous preparations. This invention also contemplates use of antibodies or binding fragments thereof which are not complement binding.

Ligand screening using cytokine receptor or fragments thereof can be performed to identify molecules having binding affinity to the receptors. Subsequent biological assays can then be utilized to determine if a putative ligand can provide competitive binding, which can block intrinsic stimulating activity. Receptor fragments can be used as a blocker or antagonist in that it blocks the activity of ligand. Likewise, a compound having intrinsic stimulating activity can activate the receptor and is thus an agonist in that it simulates the activity of ligand, e.g., inducing signaling. This invention further contemplates the therapeutic use of antibodies to cytokine receptors as antagonists.

The quantities of reagents necessary for effective therapy will depend upon many different factors, including means of administration, target site, reagent physiological life, pharmacological life, physiological state of the patient, and other medicants administered. Thus, treatment dosages should be titrated to optimize safety and efficacy. Typically,

dosages used in vitro may provide useful guidance in the amounts useful for in situ administration of these reagents. Animal testing of effective doses for treatment of particular disorders will provide further predictive indication of human dosage. Various considerations are described, e.g., in Gilman, et al. (eds. 1990) Goodman and Gilman's: The Pharmacological Bases of Therapeutics, 8th Ed., Pergamon Press; and Remington's Pharmaceutical Sciences, 17th ed. (1990), Mack Publishing Co., Easton, Penn.; each of which is hereby incorporated herein by reference. Methods for administration are discussed therein and below, e.g., for oral, intravenous, intraperitoneal, or intramuscular administration, transdermal diffusion, and others. Pharmaceutically acceptable carriers will include water, saline, buffers, and other compounds described, e.g., in the Merck Index, Merck & Co., Rahway, New Jersey. Because of the likely high affinity binding, or turnover numbers, between a putative ligand and its receptors, low dosages of these reagents would be initially expected to be effective. And the signaling pathway suggests extremely low amounts of ligand may have effect. Thus, dosage ranges would ordinarily be expected to be in amounts lower than 1 mM concentrations, typically less than about 10 μM concentrations, usually less than about 100 nM, preferably less than about 10 pM (picomolar), and most preferably less than about 1 fM (femtomolar), with an appropriate carrier. Slow release formulations, or slow release apparatus will often be utilized for continuous administration.

Cytokine receptors, fragments thereof, and antibodies or its fragments, antagonists, and agonists, may be administered directly to the host to be treated or, depending on the size of the compounds, it may be desirable to conjugate them to carrier proteins such as ovalbumin or serum albumin prior to their administration. Therapeutic formulations may be administered in many conventional dosage formulations. While it is possible for the active ingredient to be administered alone, it is preferable to present it as a pharmaceutical formulation. Formulations comprise at least one active ingredient, as defined above, together with one or more acceptable carriers thereof. Each carrier must be both pharmaceutically and physiologically acceptable in the sense of being compatible with the other ingredients and not injurious to the patient. Formulations include those suitable for oral, rectal, nasal, or parenteral (including subcutaneous, intramuscular, intravenous and intradermal) administration. The formulations may conveniently be presented in unit dosage form and may be prepared by methods well known in the art of pharmacy. See, e.g., Gilman, et al. (eds. 1990) Goodman and Gilman's: The Pharmacological Bases of Therapeutics, 8th Ed., Pergamon Press; and Remington's Pharmaceutical Sciences, 17th ed. (1990), Mack Publishing Co., Easton, Penn.; Avis, et al. (eds. 1993) Pharmaceutical Dosage Forms: Parenteral Medications Dekker, NY; Lieberman, et al. (eds. 1990) Pharmaceutical Dosage Forms: Tablets Dekker, NY; and

Lieberman, et al. (eds. 1990) Pharmaceutical Dosage Forms: Disperse Systems Dekker, NY. The therapy of this invention may be combined with or used in association with other therapeutic agents, particularly agonists or antagonists of other cytokine receptor family members.

IX. Screening

Drug screening using DCRS8 or fragments thereof can be performed to identify compounds having binding affinity to the receptor subunit, including isolation of associated components. Subsequent biological assays can then be utilized to determine if the compound has intrinsic stimulating activity and is therefore a blocker or antagonist in that it blocks the activity of the ligand. Likewise, a compound having intrinsic stimulating activity can activate the receptor and is thus an agonist in that it simulates the activity of a cytokine ligand. This invention further contemplates the therapeutic use of antibodies to the receptor as cytokine agonists or antagonists.

Similarly, complexes comprising multiple proteins may be used to screen for ligands or reagents capable of recognizing the complex. Most cytokine receptors comprise at least two subunits, which may be the same, or distinct. Alternatively, the transmembrane receptor may bind to a complex comprising a cytokine-like ligand associated with another soluble protein serving, e.g., as a second receptor subunit.

One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant DNA molecules expressing the DCRS8 in combination with another cytokine receptor subunit. Cells may be isolated which express a receptor in isolation from other functional receptors. Such cells, either in viable or fixed form, can be used for standard antibody/antigen or ligand/receptor binding assays. See also, Parce, et al. (1989) Science 246:243-247; and Owicki, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:4007-4011, which describe sensitive methods to detect cellular responses. Competitive assays are particularly useful, where the cells (source of putative ligand) are contacted and incubated with a labeled receptor or antibody having known binding affinity to the ligand, such as ^{125}I-antibody, and a test sample whose binding affinity to the binding composition is being measured. The bound and free labeled binding compositions are then separated to assess the degree of ligand binding. The amount of test compound bound is inversely proportional to the amount of labeled receptor binding to the known source. Many techniques can be used to separate bound from free ligand to assess the degree of ligand binding. This separation step could typically involve a procedure such as adhesion to filters followed by washing, adhesion to plastic followed by washing, or centrifugation of the cell membranes. Viable cells could also be used to screen for the effects of drugs on cytokine mediated functions, e.g., second messenger

levels, e.g., Ca^{++}; cell proliferation; inositol phosphate pool changes; and others. Some detection methods allow for elimination of a separation step, e.g., a proximity sensitive detection system. Calcium sensitive dyes will be useful for detecting Ca^{++} levels, with a fluorimeter or a fluorescence cell sorting apparatus.

X. Ligands

The descriptions of the DCRS8 herein provides means to identify ligands, as described above. Such ligand should bind specifically to the respective receptor with reasonably high affinity. Various constructs are made available which allow either labeling of the receptor to detect its ligand. For example, directly labeling cytokine receptor, fusing onto it markers for secondary labeling, e.g., FLAG or other epitope tags, etc., will allow detection of receptor. This can be histological, as an affinity method for biochemical purification, or labeling or selection in an expression cloning approach. A two-hybrid selection system may also be applied making appropriate constructs with the available cytokine receptor sequences. See, e.g., Fields and Song (1989) Nature 340:245-246.

Most likely candidates will be structually related to members of the IL-17 family. See, e.g., USSN 09/480,287.

The broad scope of this invention is best understood with reference to the following examples, which are not intended to limit the inventions to the specific embodiments.

EXAMPLES

I. General Methods

Some of the standard methods are described or referenced, e.g., in Maniatis, et al. (1982) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor Press; Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual, (2d ed.), vols. 1-3, CSH Press, NY; or Ausubel, et al. (1987 and Supplements) Current Protocols in Molecular Biology, Greene/Wiley, New York. Methods for protein purification include such methods as ammonium sulfate precipitation, column chromatography, electrophoresis, centrifugation, crystallization, and others. See, e.g., Ausubel, et al. (1987 and periodic supplements); Coligan, et al. (ed. 1996) and periodic supplements, Current Protocols In Protein Science Greene/Wiley, New York; Deutscher (1990) "Guide to Protein Purification" in Methods in Enzymology, vol. 182, and other volumes in this series; and manufacturer's literature on use of protein purification products, e.g., Pharmacia, Piscataway, N.J., or Bio-Rad, Richmond, CA. Combination

with recombinant techniques allow fusion to appropriate segments, e.g., to a FLAG sequence or an equivalent which can be fused via a protease-removable sequence. See, e.g., Hochuli (1990) "Purification of Recombinant Proteins with Metal Chelate Absorbent" in Setlow (ed.) Genetic Engineering, Principle and Methods 12:87-98, Plenum Press, N.Y.; and Crowe, et al. (1992) QIAexpress: The High Level Expression & Protein Purification System QUIAGEN, Inc., Chatsworth, CA.

Computer sequence analysis is performed, e.g., using available software programs, including those from the GCG (U. Wisconsin) and GenBank sources. Public sequence databases were also used, e.g., from GenBank and others.

Many techniques applicable to IL-10 receptors may be applied to the DCRSs, as described, e.g., in USSN 08/110,683 (IL-10 receptor), which is incorporated herein by reference.

II. Computational Analysis

Human sequences related to cytokine receptors were identified from genomic sequence database using, e.g., the BLAST server (Altschul, et al. (1994) Nature Genet. 6:119-129). Standard analysis programs may be used to evaluate structure, e.g., PHD (Rost and Sander (1994) Proteins 19:55-72) and DSC (King and Sternberg (1996) Protein Sci. 5:2298-2310). Standard comparison software includes, e.g., Altschul, et al. (1990) J. Mol. Biol. 215:403-10; Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chapman & Hall; Lander and Waterman (eds. 1995) Calculating the Secrets of Life: Applications of the Mathematical Sciences in Molecular Biology National Academy Press; and Speed and Waterman (eds. 1996) Genetic Mapping and DNA Sequencing (IMA Volumes in Mathematics and Its Applications, Vol 81) Springer Verlag. Each reference is incorporate herein by reference.

III. Cloning of full-length cDNAs; Chromosomal localization

PCR primers derived from the sequences are used to probe a human cDNA library. Sequences may be derived, e.g., from Tables 1-5, preferably those adjacent the ends of sequences. Full length cDNAs for primate, rodent, or other species DCRS8 are cloned, e.g., by DNA hybridization screening of λgt10 phage. PCR reactions are conducted using T. aquaticus Taqplus DNA polymerase (Stratagene) under appropriate conditions. Extending partial length cDNA clones is typically routine.

Chromosome spreads are prepared. In situ hybridization is performed on chromosome preparations obtained from phytohemagglutinin-stimulated human lymphocytes cultured for 72 h. 5-bromodeoxyuridine was added for the final seven hours

of culture (60 μg/ml of medium), to ensure a posthybridization chromosomal banding of good quality.

A PCR fragment, amplified with the help of primers, is cloned into an appropriate vector. The vector is labeled by nick-translation with ^3H. The radiolabeled probe is hybridized to metaphase spreads at final concentration of 200 ng/ml of hybridization solution as described, e.g., in Mattei, et al. (1985) Hum. Genet. 69:327-331.

After coating with nuclear track emulsion (KODAK NTB_2), slides are exposed. To avoid any slipping of silver grains during the banding procedure, chromosome spreads are first stained with buffered Giemsa solution and metaphase photographed. R-banding is then performed by the fluorochrome-photolysis-Giemsa (FPG) method and metaphases rephotographed before analysis.

Similar appropriate methods are used for other species.

IV. Localization of mRNA

Human multiple tissue (Cat# 1, 2) and cancer cell line blots (Cat# 7757-1), containing approximately 2 μg of poly(A)$^+$ RNA per lane, are purchased from Clontech (Palo Alto, CA). Probes are radiolabeled with [α-^{32}P] dATP, e.g., using the Amersham Rediprime random primer labeling kit (RPN1633). Prehybridization and hybridizations are performed, e.g., at 65° C in 0.5 M Na_2HPO_4, 7% SDS, 0.5 M EDTA (pH 8.0). High stringency washes are conducted, e.g., at 65° C with two initial washes in 2 x SSC, 0.1% SDS for 40 min followed by a subsequent wash in 0.1 x SSC, 0.1% SDS for 20 min. Membranes are then exposed at -70° C to X-Ray film (Kodak) in the presence of intensifying screens. More detailed studies by cDNA library Southerns are performed with selected appropriate human DCRS clones to examine their expression in hemopoietic or other cell subsets.

Alternatively, two appropriate primers are selected from Tables 1-5. RT-PCR is used on an appropriate mRNA sample selected for the presence of message to produce a cDNA, e.g., a sample which expresses the gene.

Full length clones may be isolated by hybridization of cDNA libraries from appropriate tissues pre-selected by PCR signal. Northern blots can be performed.

Message for genes encoding DCRS will be assayed by appropriate technology, e.g., PCR, immunoassay, hybridization, or otherwise. Tissue and organ cDNA preparations are available, e.g., from Clontech, Mountain View, CA. Identification of sources of natural expression are useful, as described. And the identification of functional receptor subunit pairings will allow for prediction of what cells express the combination of receptor subunits which will result in a physiological responsiveness to each of the cytokine ligands.

For mouse counterpart distribution, e.g., Southern Analysis can be performed: DNA (5 μg) from a primary amplified cDNA library was digested with appropriate restriction enzymes to release the inserts, run on a 1% agarose gel and transferred to a nylon membrane (Schleicher and Schuell, Keene, NH).

Samples for mouse mRNA isolation may include: resting mouse fibroblastic L cell line (C200); Braf:ER (Braf fusion to estrogen receptor) transfected cells, control (C201); T cells, TH1 polarized (Mel14 bright, CD4+ cells from spleen, polarized for 7 days with IFN-γ and anti IL-4; T200); T cells, TH2 polarized (Mel14 bright, CD4+ cells from spleen, polarized for 7 days with IL-4 and anti-IFN-γ; T201); T cells, highly TH1 polarized (see Openshaw, et al. (1995) J. Exp. Med. 182:1357-1367; activated with anti-CD3 for 2, 6, 16 h pooled; T202); T cells, highly TH2 polarized (see Openshaw, et al. (1995) J. Exp. Med. 182:1357-1367; activated with anti-CD3 for 2, 6, 16 h pooled; T203); CD44- CD25+ pre T cells, sorted from thymus (T204); TH1 T cell clone D1.1, resting for 3 weeks after last stimulation with antigen (T205); TH1 T cell clone D1.1, 10 μg/ml ConA stimulated 15 h (T206); TH2 T cell clone CDC35, resting for 3 weeks after last stimulation with antigen (T207); TH2 T cell clone CDC35, 10 μg/ml ConA stimulated 15 h (T208); Mel14+ naive T cells from spleen, resting (T209); Mel14+ T cells, polarized to Th1 with IFN-γ/IL-12/anti-IL-4 for 6, 12, 24 h pooled (T210); Mel14+ T cells, polarized to Th2 with IL-4/anti-IFN-γ for 6, 13, 24 h pooled (T211); unstimulated mature B cell leukemia cell line A20 (B200); unstimulated B cell line CH12 (B201); unstimulated large B cells from spleen (B202); B cells from total spleen, LPS activated (B203); metrizamide enriched dendritic cells from spleen, resting (D200); dendritic cells from bone marrow, resting (D201); monocyte cell line RAW 264.7 activated with LPS 4 h (M200); bone-marrow macrophages derived with GM and M-CSF (M201); macrophage cell line J774, resting (M202); macrophage cell line J774 + LPS + anti-IL-10 at 0.5, 1, 3, 6, 12 h pooled (M203); macrophage cell line J774 + LPS + IL-10 at 0.5, 1, 3, 5, 12 h pooled(M204); aerosol challenged mouse lung tissue, Th2 primers, aerosol OVA challenge 7, 14, 23 h pooled (see Garlisi, et al. (1995) Clinical Immunology and Immunopathology 75:75-83; X206); Nippostrongulus-infected lung tissue (see Coffman, et al. (1989) Science 245:308-310; X200); total adult lung, normal (O200); total lung, rag-1 (see Schwarz, et al. (1993) Immunodeficiency 4:249-252; O205); IL-10 K.O. spleen (see Kuhn, et al. (1991) Cell 75:263-274; X201); total adult spleen, normal (O201); total spleen, rag-1 (O207); IL-10 K.O. Peyer's patches (O202); total Peyer's patches, normal (O210); IL-10 K.O. mesenteric lymph nodes (X203); total mesenteric lymph nodes, normal (O211); IL-10 K.O. colon (X203); total colon, normal (O212); NOD mouse pancreas (see Makino, et al. (1980) Jikken Dobutsu 29:1-13; X205); total thymus, rag-1 (O208); total kidney, rag-1 (O209); total heart, rag-1 (O202); total brain, rag-1 (O203);

total testes, rag-1 (O204); total liver, rag-1 (O206); rat normal joint tissue (O300); and rat arthritic joint tissue (X300).

Samples for human mRNA isolation may include, e.g.: peripheral blood mononuclear cells (monocytes, T cells, NK cells, granulocytes, B cells), resting (T100); peripheral blood mononuclear cells, activated with anti-CD3 for 2, 6, 12 h pooled (T101); T cell, TH0 clone Mot 72, resting (T102); T cell, TH0 clone Mot 72, activated with anti-CD28 and anti-CD3 for 3, 6, 12 h pooled (T103); T cell, TH0 clone Mot 72, anergic treated with specific peptide for 2, 7, 12 h pooled (T104); T cell, TH1 clone HY06, resting (T107); T cell, TH1 clone HY06, activated with anti-CD28 and anti-CD3 for 3, 6, 12 h pooled (T108); T cell, TH1 clone HY06, anergic treated with specific peptide for 2, 6, 12 h pooled (T109); T cell, TH2 clone HY935, resting (T110); T cell, TH2 clone HY935, activated with anti-CD28 and anti-CD3 for 2, 7, 12 h pooled (T111); T cells CD4+CD45RO- T cells polarized 27 days in anti-CD28, IL-4, and anti IFN-γ, TH2 polarized, activated with anti-CD3 and anti-CD28 4 h (T116); T cell tumor lines Jurkat and Hut78, resting (T117); T cell clones, pooled AD130.2, Tc783.12, Tc783.13, Tc783.58, Tc782.69, resting (T118); T cell random γδ T cell clones, resting (T119); Splenocytes, resting (B100); Splenocytes, activated with anti-CD40 and IL-4 (B101); B cell EBV lines pooled WT49, RSB, JY, CVIR, 721.221, RM3, HSY, resting (B102); B cell line JY, activated with PMA and ionomycin for 1, 6 h pooled (B103); NK 20 clones pooled, resting (K100); NK 20 clones pooled, activated with PMA and ionomycin for 6 h (K101); NKL clone, derived from peripheral blood of LGL leukemia patient, IL-2 treated (K106); NK cytotoxic clone 640-A30-1, resting (K107); hematopoietic precursor line TF1, activated with PMA and ionomycin for 1, 6 h pooled (C100); U937 premonocytic line, resting (M100); U937 premonocytic line, activated with PMA and ionomycin for 1, 6 h pooled (M101); elutriated monocytes, activated with LPS, IFNγ, anti-IL-10 for 1, 2, 6, 12, 24 h pooled (M102); elutriated monocytes, activated with LPS, IFNγ, IL-10 for 1, 2, 6, 12, 24 h pooled (M103); elutriated monocytes, activated with LPS, IFNγ, anti-IL-10 for 4, 16 h pooled (M106); elutriated monocytes, activated with LPS, IFNγ, IL-10 for 4, 16 h pooled (M107); elutriated monocytes, activated LPS for 1 h (M108); elutriated monocytes, activated LPS for 6 h (M109); DC 70% CD1a+, from CD34+ GM-CSF, TNFα 12 days, resting (D101); DC 70% CD1a+, from CD34+ GM-CSF, TNFα 12 days, activated with PMA and ionomycin for 1 hr (D102); DC 70% CD1a+, from CD34+ GM-CSF, TNFα 12 days, activated with PMA and ionomycin for 6 hr (D103); DC 95% CD1a+, from CD34+ GM-CSF, TNFα 12 days FACS sorted, activated with PMA and ionomycin for 1, 6 h pooled (D104); DC 95% CD14+, ex CD34+ GM-CSF, TNFα 12 days FACS sorted, activated with PMA and ionomycin 1, 6 hr pooled (D105); DC CD1a+ CD86+, from CD34+ GM-CSF, TNFα 12 days FACS sorted, activated with PMA and

ionomycin for 1, 6 h pooled (D106); DC from monocytes GM-CSF, IL-4 5 days, resting (D107); DC from monocytes GM-CSF, IL-4 5 days, resting (D108); DC from monocytes GM-CSF, IL-4 5 days, activated LPS 4, 16 h pooled (D109); DC from monocytes GM-CSF, IL-4 5 days, activated TNFα, monocyte supe for 4, 16 h pooled (D110); leiomyoma L11 benign tumor (X101); normal myometrium M5 (O115); malignant leiomyosarcoma GS1 (X103); lung fibroblast sarcoma line MRC5, activated with PMA and ionomycin for 1, 6 h pooled (C101); kidney epithelial carcinoma cell line CHA, activated with PMA and ionomycin for 1, 6 h pooled (C102); kidney fetal 28 wk male (O100); lung fetal 28 wk male (O101); liver fetal 28 wk male (O102); heart fetal 28 wk male (O103); brain fetal 28 wk male (O104); gallbladder fetal 28 wk male (O106); small intestine fetal 28 wk male (O107); adipose tissue fetal 28 wk male (O108); ovary fetal 25 wk female (O109); uterus fetal 25 wk female (O110); testes fetal 28 wk male (O111); spleen fetal 28 wk male (O112); adult placenta 28 wk (O113); and tonsil inflamed, from 12 year old (X100).

TaqMan quantitative PCR techniques have shown the DCRS6, in both mouse and human, to be expressed on T cells, including thymocytes and CD4+ naive and differentiated (hDCRS6 is also expressed on dendritic cells), in gastrointestinal tissue, including stomach, intestine, colon and associated lymphoid tissue, e.g., Peyer's patches and mesenteric lymph nodes, and upregulated in inflammatory models of bowel disease, e.g., IL-10 KO mice. The hDCRS7 was detected in both resting and activated dendritic cells, epithelial cells, and mucosal tissues, including GI and reproductive tracts. These data suggest that family members are expressed in mucosal tissues and immune system cell types, and/or in gastrointestinal, airway, and reproductive tract development.

As such, therapeutic indications include, e.g., short bowel syndrome, post chemo/radio-therapy or alcoholic recovery, combinations with ulcer treatments or arthritis medication, Th2 pregnancy skewing, stomach lining/tissue regeneration, loss of adsorptive surface conditions, etc. See, e.g., Yamada, et al. (eds. 1999) Textbook of Gastroenterology; Yamada, et al. (eds. 1999) Textbook and Atlas of Gastroenterology; Gore and Levine (2000) Textbook of Gastrointestinal Radiology; and (1987) Textbook of Pediatric Gastroenterology.

Similar samples may isolated in other species for evaluation.

Primers specific for IL-17RA were designed and used in Taqman quantative PCR against various human libraries. IL-17RA is highly expressed in innate immune myeloid cells including dendritic cells and monocytes. Expression is also detected in T-cell libraries. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.

Table for IL-17RA library description	CT for IL-17RA_H
DC ex monocytes GM-CSF, IL-4, resting	16.97
U937 premonocytic line, activated	17.14
DC ex monocytes GM-CSF, IL-4, resting	17.53
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, resting	18.17
monocytes, LPS, gIFN, anti-IL-10	18.27
DC ex monocytes GM-CSF, IL-4, LPS activated 4+16 hr	18.51
DC ex monocytes GM-CSF, IL-4, monokine activated 4+16 hr	18.68
kidney epithelial carcinoma cell line CHA, activated	18.69
monocytes, LPS, 1 hr	18.72
monocytes, LPS, 6 hr	18.72
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, activated 1 hr	18.91
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, activated 6 hr	18.94
T cell, TH1 clone HY06, activated	18.99
lung fetal	19.15
T cell, TH1 clone HY06, resting	19.18
T cell, TH1 clone HY06, anergic	19.23
monocytes, LPS, gIFN, IL-10, 4+16 hr	19.3
spleen fetal	19.51
testes fetal	19.7
T cell, TH0 clone Mot 72, resting	19.71
T cell, TH0 clone Mot 72, resting	19.84
DC CD1a+ CD86+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	19.94
peripheral blood mononuclear cells, activated	20.01
hematopoietic precursor line TF1, activated	20.07
lung fibroblast sarcoma line MRC5, activated	20.18
Splenocytes, activated	20.21
T cell gd clones, resting	20.27
ovary fetal	20.45
T cells CD4+, TH2 polarized, activated	20.57
Splenocytes, resting	20.6
uterus fetal	20.62
DC 95% CD1a+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	20.94
epithelial cells, unstimulated	20.96
peripheral blood mononuclear cells, resting	20.97
adipose tissue fetal	21.13

B cell line JY, activated	21.28
monocytes, LPS, gIFN, IL-10	21.37
placenta 28 wk	21.38
NK 20 clones pooled, activated	21.55
pool of two normal human lung samples	21.63
normal human thyroid	21.65
epithelial cells, IL-1b activated	21.72
normal human skin	21.84
T cell, TH0 clone Mot 72, anergic	21.87
small intestine fetal	22.01
CD28- T cell clone in pME	22.08
T cell, TH2 clone HY935, activated	22.09
T cell clones, pooled, resting	22.29
Hashimoto's thyroiditis thyroid sample	22.3
NK 20 clones pooled, resting	22.4
B cell EBV lines, resting	22.45
T cell, TH2 clone HY935, resting	22.86
T cell, TH0 clone Mot 72, activated	23.3
monocytes, LPS, gIFN, anti-IL-10, 4+16 hr	23.39
T cell lines Jurkat and Hut78, resting	23.4
T cell, TH0 clone Mot 72, activated	23.56
Pneumocystic carnii pneumonia lung sample	24.05
U937 premonocytic line, resting	25.01
pool of rheumatoid arthritis samples, human	25.85
pool of three heavy smoker human lung samples	26.1
DC 95% CD14+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	32.69
kidney fetal	33.7
liver fetal	34.4
NK cytotoxic clone, resting	34.49
tonsil inflammed	35.02
normal w.t. monkey lung	35.45
gallbladder fetal	35.84
TR1 T cell clone	35.86
allergic lung sample	36.39
Psoriasis patient skin sample	36.44
normal human colon	37.34
brain fetal	37.35
Ascaris-challenged monkey lung, 4 hr.	37.75
Ascaris-challenged monkey lung, 24 hr.	40
heart fetal	40
normal w.t. monkey colon	40
ulcerative colitis human colon sample	40

Primers specific for DCRS6_H were designed and used in Taqman quantative PCR against various human libraries. DCRS6_H is expressed in innate immune myeloid cells including dendritic cells and monocytes. Expression is also detected in T-cell libraries. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.

Table for DCRS6_H

library description	**CT for DCRS6_H**
T cell, TH0 clone Mot 72, resting	15.54
T cell, TH0 clone Mot 72, resting	15.7
DC ex monocytes GM-CSF, IL-4, resting	17.84
DC ex monocytes GM-CSF, IL-4, resting	18.19
DC ex monocytes GM-CSF, IL-4, LPS activated 4+16 hr	18.3
DC ex monocytes GM-CSF, IL-4, monokine activated 4+16 hr	18.3
T cell, TH1 clone HY06, resting	18.43
NK cytotoxic clone, resting	18.53
T cell clones, pooled, resting	18.8
T cell, TH1 clone HY06, activated	19.03
T cell, TH2 clone HY935, activated	19.1
TR1 T cell clone	19.12
T cells CD4+, TH2 polarized, activated	20.06
B cell EBV lines, resting	20.3
T cell, TH2 clone HY935, resting	20.48
kidney epithelial carcinoma cell line CHA, activated	21.07
T cell, TH1 clone HY06, anergic	21.14
normal human colon	21.29
NK 20 clones pooled, resting	21.49
T cell gd clones, resting	21.58
gallbladder fetal	22.21
kidney fetal	22.79
liver fetal	22.8
Pneumocystic carnii pneumonia lung sample	23.06
CD28- T cell clone in pME	23.18
T cell, TH0 clone Mot 72, anergic	23.2
ovary fetal	23.51
normal human thyroid	24.03
small intestine fetal	24.13
testes fetal	24.82
epithelial cells, IL-1b activated	26.08
pool of three heavy smoker human lung samples	26.49
placenta 28 wk	26.56
normal w.t. monkey lung	28.65
peripheral blood mononuclear cells,	33.39

activated	
Ascaris-challenged monkey lung, 4 hr.	36.59
spleen fetal	38.43
peripheral blood mononuclear cells, resting	40
T cell, TH0 clone Mot 72, activated	40
T cell lines Jurkat and Hut78, resting	40
Splenocytes, resting	40
Splenocytes, activated	40
B cell line JY, activated	40
NK 20 clones pooled, activated	40
hematopoietic precursor line TF1, activated	40
U937 premonocytic line, resting	40
U937 premonocytic line, activated	40
monocytes, LPS, gIFN, anti-IL-10	40
monocytes, LPS, gIFN, IL-10	40
monocytes, LPS, gIFN, anti-IL-10, 4+16 hr	40
monocytes, LPS, gIFN, IL-10, 4+16 hr	40
monocytes, LPS, 1 hr	40
monocytes, LPS, 6 hr	40
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, resting	40
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, activated 1 hr	40
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, activated 6 hr	40
DC 95% CD1a+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	40
DC 95% CD14+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	40
DC CD1a+ CD86+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	40
epithelial cells, unstimulated	40
lung fibroblast sarcoma line MRC5, activated	40
Ascaris-challenged monkey lung, 24 hr.	40
pool of two normal human lung samples	40
allergic lung sample	40
normal w.t. monkey colon	40
ulcerative colitis human colon sample	40
Hashimoto's thyroiditis thyroid sample	40
pool of rheumatoid arthritis samples, human	40
normal human skin	40
Psoriasis patient skin sample	40
tonsil inflammed	40
lung fetal	40
heart fetal	40
brain fetal	40
adipose tissue fetal	40
uterus fetal	40

T cell, TH0 clone Mot 72, activated	40

Primers specific for DCRS7_H were designed and used in Taqman quantative PCR against various human libraries. DCRS7_H is expressed in innate immune myeloid cells including dendritic cells and monocytes. Expression is also detected in fetal libraries. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.

Table for DCRS7_H

library description	**CT for DCRS7_H**
fetal uterus	19.05
DC mix	19.34
fetal small intestine	19.46
fetal ovary	19.68
fetal testes	19.75
fetal lung	20.04
CHA	20.24
normal thyroid	20.32
DC/GM/IL-4	20.52
fetal spleen	20.86
normal lung	20.94
TF1	21
allergic lung #19	21.02
Psoriasis skin	21.07
fetal liver	21.15
MRC5	21.15
24 hr. Ascaris lung	21.17
hi dose IL-4 lung	21.23
CD1a+ 95%	21.32
Hashimotos thyroiditis	21.35
Crohns colon 4003197A	21.35
normal lung pool	21.36
70% DC resting	21.42
fetal kidney	21.58
adult placenta	21.68
lung 121897-1	21.8
Pneumocystis carnii lung #20	21.81
A549 unstim.	21.89
normal colon #22	21.94
18 hr. Ascaris lung	22.09
normal skin	22.1
Crohns colon 9609C144	22.13
fetal adipose tissue	22.35
D6	22.39

DC resting CD34-derived	22.45
DC TNF/TGFb act CD34-der.	22.54
fetal brain	22.9
DC CD40L activ. mono-deriv.	22.91
Crohns colon 403242A	22.91
ulcerative colitis colon #26	23
RA synovium pool	23.06
A549 activated	23.06
mono + IL-10	23.42
DC LPS	23.49
Mot 72 activated	23.66
CD1a+ CD86+	23.86
HY06 resting	23.87
U937 activated	23.97
inflammed tonsil	23.97
D1	24.06
M1	24.17
CD14+ 95%	24.21
lung 080698-2	24.28
4 hr. Ascaris lung	24.37
Jurkat activated pSPORT	24.42
DC resting mono-derived	24.48
HY06 activated	24.54
C+	24.64
Splenocytes resting	24.65
U937/CD004 resting	24.96
PBMC resting	25.8
Mot 72 resting	25.91
mono + anti-IL-10	26.14
NK pool	26.99
HY06 anti-peptide	27.34
mast cell pME	27.38
Tc gamma delta	28.14
TC1080 CD28- pMET7	31.05
PBMC activated	31.89
NK non cytotox.	32.3
RV-C30 TR1 pMET7	32.5
Bc	33.72
C-	33.8
Splenocytes activated	34.7
JY	35.05
NK cytotox.	36.44
NKL/IL-2	37.59
HY935 resting	37.6
NK pool activated	38.15
Mot 72 anti-peptide	38.87
fetal heart	40.92

B21 resting	42.05
Jurkat resting pSPORT	42.8
B21 activated	43.09
NKA6 pSPORT	44.85
HY935 activated	45
M6	45

Primers specific for DCRS9_H were designed and used in Taqman quantative PCR against various human libraries. DCRS9_H is expressed T-cells, fetal lung, and resting monocytes. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.

Table for DCRS9_H

library description	**CT for DCRS9_H**
HY06 resting	22.35
fetal lung	22.63
HY06 anti-peptide	22.72
HY06 activated	22.96
U937/CD004 resting	24.16
fetal small intestine	24.94
JY	25.04
Mot 72 resting	25.12
Jurkat activated pSPORT	25.2
RV-C30 TR1 pMET7	26.51
fetal kidney	26.76
MRC5	27.2
Psoriasis skin	27.3
Tc gamma delta	27.37
Crohns colon 4003197A	27.44
fetal spleen	27.72
normal lung	27.83
Hashimotos thyroiditis	28.03
B21 resting	28.32
TF1	28.39
NK cytotox.	28.44
TC1080 CD28- pMET7	28.61
Pneumocystis carnii lung #20	29.05
U937 activated	29.06
HY935 resting	29.09
CD1a+ 95%	29.13

B21 activated	29.2
Mot 72 activated	29.21
fetal testes	29.27
lung 080698-2	29.32
Jurkat resting pSPORT	29.38
CD14+ 95%	29.38
normal thyroid	29.53
Mot 72 anti-peptide	29.65
Splenocytes resting	29.85
Crohns colon 9609C144	30.28
lung 121897-1	30.37
24 hr. Ascaris lung	30.59
hi dose IL-4 lung	30.8
CD1a+ CD86+	31.42
normal skin	31.73
fetal uterus	31.79
PBMC activated	31.82
inflammed tonsil	31.98
fetal brain	32.21
RA synovium pool	32.77
allergic lung #19	33.18
18 hr. Ascaris lung	33.42
adult placenta	33.43
normal lung pool	33.45
Crohns colon 403242A	33.52
NK pool	33.72
HY935 activated	33.75
DC/GM/IL-4	34.28
DC resting mono-derived	34.57
fetal ovary	35.06
fetal adipose tissue	35.07
CHA	35.2
PBMC resting	35.95
Bc	36.19
A549 unstim.	36.4
fetal heart	36.87
ulcerative colitis colon #26	37.83
C-	38.32
4 hr. Ascaris lung	40.2
D6	40.62
C+	44.38

A549 activated	44.58
Splenocytes activated	45
NK pool activated	45
NKA6 pSPORT	45
NKL/IL-2	45
NK non cytotox.	45
mono + anti-IL-10	45
mono + IL-10	45
M1	45
M6	45
70% DC resting	45
D1	45
DC LPS	45
DC mix	45
fetal liver	45
mast cell pME	45
DC CD40L activ. mono-deriv.	45
DC resting CD34-derived	45
DC TNF/TGFb act CD34-der.	45
normal colon #22	45

V. Cloning of species counterparts

Various strategies are used to obtain species counterparts of the DCRSs, preferably from other primates or rodents. One method is by cross hybridization using closely related species DNA probes. It may be useful to go into evolutionarily similar species as intermediate steps. Another method is by using specific PCR primers based on the identification of blocks of similarity or difference between genes, e.g., areas of highly conserved or nonconserved polypeptide or nucleotide sequence. Sequence database searches may identify species counterparts.

VI. Production of mammalian protein

An appropriate, e.g., GST, fusion construct is engineered for expression, e.g., in E. coli. For example, a mouse IGIF pGex plasmid is constructed and transformed into E. coli. Freshly transformed cells are grown, e.g., in LB medium containing 50 μg/ml ampicillin and induced with IPTG (Sigma, St. Louis, MO). After overnight induction, the bacteria are harvested and the pellets containing the appropriate protein are isolated. The pellets are homogenized, e.g., in TE buffer (50 mM Tris-base pH 8.0, 10 mM EDTA and 2 mM pefabloc) in 2 liters. This material is passed through a microfluidizer (Microfluidics, Newton, MA) three times. The fluidized supernatant is spun down on a Sorvall GS-3 rotor for 1 h at 13,000 rpm. The resulting supernatant containing the cytokine receptor protein is filtered and passed over a glutathione-SEPHAROSE column equilibrated in 50 mM Tris-base pH 8.0. Fractions containing the DCRS8-GST fusion protein are pooled and cleaved, e.g., with thrombin (Enzyme Research Laboratories, Inc., South Bend, IN). The cleaved pool is then passed over a Q-SEPHAROSE column equilibrated in 50 mM Tris-base. Fractions containing DCRS8 are pooled and diluted in cold distilled H_2O, to lower the conductivity, and passed back over a fresh Q-Sepharose column, alone or in succession with an immunoaffinity antibody column. Fractions containing the DCRS8 protein are pooled, aliquoted, and stored in the -70° C freezer.

Comparison of the CD spectrum with cytokine receptor protein may suggest that the protein is correctly folded. See Hazuda, et al. (1969) J. Biol. Chem. 264:1689-1693.

VII. Preparation of specific antibodies

Inbred Balb/c mice are immunized intraperitoneally with recombinant forms of the protein, e.g., purified DCRS8 or stable transfected NIH-3T3 cells. Animals are boosted at appropriate time points with protein, with or without additional adjuvant, to further stimulate antibody production. Serum is collected, or hybridomas produced with harvested spleens.

Alternatively, Balb/c mice are immunized with cells transformed with the gene or fragments thereof, either endogenous or exogenous cells, or with isolated membranes enriched for expression of the antigen. Serum is collected at the appropriate time, typically after numerous further administrations. Various gene therapy techniques may be useful, e.g., in producing protein in situ, for generating an immune response. Serum or antibody preparations may be cross-absorbed or immunoselected to prepare substantially purified antibodies of defined specificity and high affinity.

Monoclonal antibodies may be made. For example, splenocytes are fused with an appropriate fusion partner and hybridomas are selected in growth medium by standard procedures. Hybridoma supernatants are screened for the presence of antibodies which bind to the DCRS8, e.g., by ELISA or other assay. Antibodies which specifically recognize specific DCRS8 embodiments may also be selected or prepared.

In another method, synthetic peptides or purified protein are presented to an immune system to generate monoclonal or polyclonal antibodies. See, e.g., Coligan (ed. 1991) Current Protocols in Immunology Wiley/Greene; and Harlow and Lane (1989) Antibodies: A Laboratory Manual Cold Spring Harbor Press. In appropriate situations, the binding reagent is either labeled as described above, e.g., fluorescence or otherwise, or immobilized to a substrate for panning methods. Nucleic acids may also be introduced into cells in an animal to produce the antigen, which serves to elicit an immune response. See, e.g., Wang, et al. (1993) Proc. Nat'l. Acad. Sci. 90:4156-4160; Barry, et al. (1994) BioTechniques 16:616-619; and Xiang, et al. (1995) Immunity 2: 129-135.

VIII. Production of fusion proteins

Various fusion constructs are made with DCRS8 or DCRS9. A portion of the appropriate gene is fused to an epitope tag, e.g., a FLAG tag, or to a two hybrid system construct. See, e.g., Fields and Song (1989) Nature 340:245-246.

The epitope tag may be used in an expression cloning procedure with detection with anti-FLAG antibodies to detect a binding partner, e.g., ligand for the respective cytokine receptor. The two hybrid system may also be used to isolate proteins which specifically bind to the receptor subunit.

IX. Structure activity relationship

Information on the criticality of particular residues is determined using standard procedures and analysis. Standard mutagenesis analysis is performed, e.g., by generating many different variants at determined positions, e.g., at the positions identified above, and evaluating biological activities of the variants. This may be performed to the extent of determining positions which modify activity, or to focus on specific positions to

determine the residues which can be substituted to either retain, block, or modulate biological activity.

Alternatively, analysis of natural variants can indicate what positions tolerate natural mutations. This may result from populational analysis of variation among individuals, or across strains or species. Samples from selected individuals are analyzed, e.g., by PCR analysis and sequencing. This allows evaluation of population polymorphisms.

X. Isolation of a ligand

A cytokine receptor can be used as a specific binding reagent to identify its binding partner, by taking advantage of its specificity of binding, much like an antibody would be used. The binding receptor may be a heterodimer of receptor subunits; or may involve, e.g., a complex of the DCRS8 with another cytokine receptor subunit. A binding reagent is either labeled as described above, e.g., fluorescence or otherwise, or immobilized to a substrate for panning methods.

The binding composition is used to screen an expression library made from a cell line which expresses a binding partner, i.e., ligand, preferably membrane associated. Standard staining techniques are used to detect or sort surface expressed ligand, or surface expressing transformed cells are screened by panning. Screening of intracellular expression is performed by various staining or immunofluorescence procedures. See also McMahan, et al. (1991) EMBO J. 10:2821-2832.

For example, on day 0, precoat 2-chamber permanox slides with 1 ml per chamber of fibronectin, 10 ng/ml in PBS, for 30 min at room temperature. Rinse once with PBS. Then plate COS cells at 2-3 x 10^5 cells per chamber in 1.5 ml of growth media. Incubate overnight at 37 C.

On day 1 for each sample, prepare 0.5 ml of a solution of 66 µg/ml DEAE-dextran, 66 µM chloroquine, and 4 µg DNA in serum free DME. For each set, a positive control is prepared, e.g., of DCRS8-FLAG cDNA at 1 and 1/200 dilution, and a negative mock. Rinse cells with serum free DME. Add the DNA solution and incubate 5 hr at 37 C. Remove the medium and add 0.5 ml 10% DMSO in DME for 2.5 min. Remove and wash once with DME. Add 1.5 ml growth medium and incubate overnight.

On day 2, change the medium. On days 3 or 4, the cells are fixed and stained. Rinse the cells twice with Hank's Buffered Saline Solution (HBSS) and fix in 4% paraformaldehyde (PFA)/glucose for 5 min. Wash 3X with HBSS. The slides may be stored at -80 C after all liquid is removed. For each chamber, 0.5 ml incubations are performed as follows. Add HBSS/saponin (0.1%) with 32 µl/ml of 1 M NaN_3 for 20 min. Cells are then washed with HBSS/saponin 1X. Add appropriate DCRS8 or

DCRS8/antibody complex to cells and incubate for 30 min. Wash cells twice with HBSS/saponin. If appropriate, add first antibody for 30 min. Add second antibody, e.g., Vector anti-mouse antibody, at 1/200 dilution, and incubate for 30 min. Prepare ELISA solution, e.g., Vector Elite ABC horseradish peroxidase solution, and preincubate for 30 min. Use, e.g., 1 drop of solution A (avidin) and 1 drop solution B (biotin) per 2.5 ml HBSS/saponin. Wash cells twice with HBSS/saponin. Add ABC HRP solution and incubate for 30 min. Wash cells twice with HBSS, second wash for 2 min, which closes cells. Then add Vector diaminobenzoic acid (DAB) for 5 to 10 min. Use 2 drops of buffer plus 4 drops DAB plus 2 drops of H_2O_2 per 5 ml of glass distilled water. Carefully remove chamber and rinse slide in water. Air dry for a few minutes, then add 1 drop of Crystal Mount and a cover slip. Bake for 5 min at 85-90 C.

Evaluate positive staining of pools and progressively subclone to isolation of single genes responsible for the binding.

Alternatively, receptor reagents are used to affinity purify or sort out cells expressing a putative ligand. See, e.g., Sambrook, et al. or Ausubel, et al.

Another strategy is to screen for a membrane bound receptor by panning. The receptor cDNA is constructed as described above. Immobilization may be achieved by use of appropriate antibodies which recognize, e.g., a FLAG sequence of a DCRS8 fusion construct, or by use of antibodies raised against the first antibodies. Recursive cycles of selection and amplification lead to enrichment of appropriate clones and eventual isolation of receptor expressing clones.

Phage expression libraries can be screened by mammalian DCRS8. Appropriate label techniques, e.g., anti-FLAG antibodies, will allow specific labeling of appropriate clones.

We tested the ability of DCRS receptors to specifically bind IL-17 family cytokines. Recombinant FLAG-hIL-17 family cytokines were used in binding experiments on Baf/3 DCRS receptor transfected expressing recombinant IL-17R_H, DCRS6_H, DCRS7_H, DCRS8_H and DCRS9_H and analyzed by FACS. We can demonstrate specific binding of IL-17 family member IL-74 to DCRS6 expressing Baf/3 cells. In additional experiments we have shown IL-17 specific binding to IL-17R_H, DCRS7_H, DCRS8_H. Further experiments show IL-71 binding to DCRS8_Hu transfectants. These experiments demonstrate the sequence homology among IL-17 related cytokine receptors confers functional binding to IL-17 cytokines.

All citations herein are incorporated herein by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Many modifications and variations of this invention can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. The specific embodiments described herein are offered by way of example only, and the invention is to be limited by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled; and the invention is not to be limited by the specific embodiments that have been presented herein by way of example.

WHAT IS CLAIMED IS:

1. A composition of matter selected from:

a) a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 14;

b) a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 14;

c) a natural sequence DCRS8 comprising mature SEQ ID NO: 14;

d) a fusion polypeptide comprising DCRS8 sequence;

e) a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 17 or 20;

f) a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 17 or 20;

g) a natural sequence DCRS9 comprising mature SEQ ID NO: 17 or 20; or

h) a fusion polypeptide comprising DCRS9 sequence.

2. The substantially pure or isolated antigenic polypeptide of Claim 1, wherein said distinct nonoverlapping segments of identity include:

a) one of at least eight amino acids;

b) one of at least four amino acids and a second of at least five amino acids;

c) at least three segments of at least four, five, and six amino acids, or

d) one of at least twelve amino acids.

3. The composition of matter of Claim 1, wherein said:

a) polypeptide:

i) comprises a mature sequence of Table 3 or 4;

ii) is an unglycosylated form of DCRS8 or DCRS9;

iii) is from a primate, such as a human;

iv) comprises at least seventeen amino acids of SEQ ID NO: 14 or 17;

v) exhibits at least four nonoverlapping segments of at least seven amino acids of SEQ ID NO: 14 or 17;

vi) is a natural allelic variant of DCRS8 or DCRS9;

vii) has a length at least about 30 amino acids;

viii) exhibits at least two non-overlapping epitopes which are specific for a primate DCRS8 or DCRS9;
ix) is glycosylated;
x) has a molecular weight of at least 30 kD with natural glycosylation;
xi) is a synthetic polypeptide;
xii) is attached to a solid substrate;
xiii) is conjugated to another chemical moiety;
xiv) is a 5-fold or less substitution from natural sequence; or
xv) is a deletion or insertion variant from a natural sequence.

4. A composition comprising:
a) a substantially pure DCRS8 or DCRS9 and another cytokine receptor family member;
b) a sterile DCRS8 or DCRS9 polypeptide of Claim 1;
c) said DCRS8 or DCRS9 polypeptide of Claim 1 and a carrier, wherein said carrier is:
i) an aqueous compound, including water, saline, and/or buffer; and/or
ii) formulated for oral, rectal, nasal, topical, or parenteral administration.

5. The fusion polypeptide of Claim 1, comprising:
a) mature protein sequence of Table 3 or 4;
b) a detection or purification tag, including a FLAG, His6, or Ig sequence; or
c) sequence of another cytokine receptor protein.

6. A kit comprising a polypeptide of Claim 1, and:
a) a compartment comprising said protein or polypeptide; or
b) instructions for use or disposal of reagents in said kit.

7. A binding compound comprising an antigen binding site from an antibody, which specifically binds to a natural DCRS8 or DCRS9 polypeptide of Claim 1, wherein:
a) said binding compound is in a container;
b) said DCRS8 or DCRS9 polypeptide is from a human;
c) said binding compound is an Fv, Fab, or Fab2 fragment;
d) said binding compound is conjugated to another chemical moiety; or
e) said antibody:
i) is raised against a peptide sequence of a mature polypeptide of Table 3 or 4;

ii) is raised against a mature DCRS8 or DCRS9;
iii) is raised to a purified human DCRS8 or DCRS9;
iv) is immunoselected;
v) is a polyclonal antibody;
vi) binds to a denatured DCRS8 or DCRS9;
vii) exhibits a Kd to antigen of at least 30 µM;
viii) is attached to a solid substrate, including a bead or plastic membrane;
ix) is in a sterile composition; or
x) is detectably labeled, including a radioactive or fluorescent label.

8. A kit comprising said binding compound of Claim 7, and:
a) a compartment comprising said binding compound; or
b) instructions for use or disposal of reagents in said kit.

9. A method of producing an antigen:antibody complex, comprising contacting under appropriate conditions a primate DCRS8 or DCRS9 polypeptide with an antibody of Claim 7, thereby allowing said complex to form.

10. The method of Claim 9, wherein:
a) said complex is purified from other cytokine receptors;
b) said complex is purified from other antibody;
c) said contacting is with a sample comprising an interferon;
d) said contacting allows quantitative detection of said antigen;
e) said contacting is with a sample comprising said antibody; or
f) said contacting allows quantitative detection of said antibody.

11. A composition comprising:
a) a sterile binding compound of Claim 7, or
b) said binding compound of Claim 7 and a carrier, wherein said carrier is:
i) an aqueous compound, including water, saline, and/or buffer; and/or
ii) formulated for oral, rectal, nasal, topical, or parenteral administration.

12. An isolated or recombinant nucleic acid encoding said polypeptide of Claim 1, wherein said:
a) DCRS8 or DCRS9 is from a human; or
b) said nucleic acid:
i) encodes an antigenic peptide sequence of Table 3 or 4;

ii) encodes a plurality of antigenic peptide sequences of Table 3 or 4;
iii) exhibits identity over at least thirteen nucleotides to a natural cDNA encoding said segment;
iv) is an expression vector;
v) further comprises an origin of replication;
vi) is from a natural source;
vii) comprises a detectable label;
viii) comprises synthetic nucleotide sequence;
ix) is less than 6 kb, preferably less than 3 kb;
x) is from a primate;
xi) comprises a natural full length coding sequence;
xii) is a hybridization probe for a gene encoding said DCRS8 or DCRS9; or
xiii) is a PCR primer, PCR product, or mutagenesis primer.

13. A cell or tissue comprising said recombinant nucleic acid of Claim 12.

14. The cell of Claim 13, wherein said cell is:
a) a prokaryotic cell;
b) a eukaryotic cell;
c) a bacterial cell;
d) a yeast cell;
e) an insect cell;
f) a mammalian cell;
g) a mouse cell;
h) a primate cell; or
i) a human cell.

15. A kit comprising said nucleic acid of Claim 12, and:
a) a compartment comprising said nucleic acid;
b) a compartment further comprising a primate DCRS8 or DCRS9 polypeptide; or
c) instructions for use or disposal of reagents in said kit.

16. A nucleic acid which:
a) hybridizes under wash conditions of 30 minutes at 30° C and less than 2M salt to the coding portion of SEQ ID NO: 13 or 16; or

b) exhibits identity over a stretch of at least about 30 nucleotides to a primate DCRS8 or DCRS9.

17. The nucleic acid of Claim 16, wherein:
a) said wash conditions are at 45° C and/or 500 mM salt; or
b) said stretch is at least 55 nucleotides.

18. The nucleic acid of Claim 16, wherein:
a) said wash conditions are at 55° C and/or 150 mM salt; or
b) said stretch is at least 75 nucleotides.

19. A method of modulating physiology or development of a cell or tissue culture cells comprising contacting said cell with an agonist or antagonist of a mammalian DCRS8 or DCRS9.

20. The method of Claim 19, wherein said cell is transformed with a nucleic acid encoding said DCRS8 or DCRS9 and another cytokine receptor subunit.

```
DCRS7_Mu     RTALLLHSADG-AGYERLVGALASALSQMP---LRVAVDLWSRRE-LSAHGALAWFHHQR
DCRS7_Hu     RAALLLYSADD-SGFERLVGALASALCQLP---LRVAVDLWSRRE-LSAQGPVAWFHAQR
IL-17R_Hu    RKVWIIYSADH-PLYVDVVLKFAQFLLTACG--TEVALDLLEEQA-ISEAGVMTWVGRQK
IL-17R_Mu    RKVWIVYSADH-PLYVEVVLKFAQFLITACG--TEVALDLLEEQV-ISEVGVMTWVSRQK
DCRS10       RKVFITYSMD----TAMEVVKFVNFLLVNG---FQTAIDIFEDR--IRGIDIIKWMERYL
DCRS10_Mu    RKVFITYSMD----TAMEVVKFVNFLLVNG---FQTAIDIFEDR--IRGIDIIKWMERYL
DCRS9_Hu     RPVLLLHAADS-EAQRRLVGALAELLRAALGGGRDVIVDLWEGRH-VARVGPLPWLWAAR
DCRS8_Hu     PKVFLCYSSKDGQNHMNVVQCFAYFLQDFCG--CEVALDLWEDFS-LCREGQREWVIQKI
IL-17R_Ce    VKVMIVYADDN-DLHTDCVKKLVENLRNCAS--CDPVFDLEKLI--TAEIVPSRWLVDQI
DCRS6_Hu     IKVLVVYPSEI--CFHHTICYFTEFLQNHCR--SEVILEKWQKKK-IAEMGPVQWLATQK
DCRS6_Ce     FKVMLVCPEVS-GRDEDFMMRIADALKKSN---NKVVCDRWFEDSKNAEENMLHWVYEQT
               . :  .              :  : .  *                   :                *.

DCRS7_Mu     RRILQEGGVVILLFSPAAVAQCQ---QWLQLQTVEP---GP---HDALAAWLSCVLPDFL
DCRS7_Hu     RQTLQEGGVVVLLFSPGAVALCS---EWLQDGVSGPGAHGP---HDAFRASLSCVLPDFL
IL-17R_Hu    QEMVESNSKIIVLCSRGTRAKWQALLGRGAP-VRLRCDHGKPV-GDLFTAAMNMILPDFK
IL-17R_Mu    QEMVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHWKPA-GDLFTAAMNMILPDFK
DCRS10       R---DKTVMIIVAISPKYKQDVE----GAESQLDED-EHGL---HTKYIHRM-MQIEFIK
DCRS10_Mu    R---DKTVMIIVAISPKYKQDVE----GAESQLDED-EHGL---HTKYIHRM-MQIEFIS
DCRS9_Hu     TRVAREQGTVLLLWSGADLRPVS----GPDP-RAAP----------LLA----LLHAAP
DCRS8_Hu     H----ESQFIIVVCSKGMKYFVD---KKNYKHKGGGRGSGK---GELFLVAVSAIAEKLR
IL-17R_Ce    S----SLKKFIIVVSDCAEKILD----TEASETHQLVQARP--FADLFGPAMEMIIRDAT
DCRS6_Hu     K----AADKVVFLLSNDVNSVCD----GTCGKSEGSPSENS---QDLFPLAFNLFCSDLR
DCRS6_Ce     K----IAEKIIVFHSAYYHPRCG---IYDVINNFFPCTDPR-----LAHIALT---PEAQ
                     .:.   *
```

FIG. 1A

```
DCRS7_Mu      QGRATGR-----YVGVYFDGLLHPDSVPSPFRVAPLFSLP-SQLPAFLDALQ--GGCSTS
DCRS7_Hu      QGRAPGS-----YVGACFDRLLHPDAVPALFRTVPVFTLP-SQLPDFLGALQ--QPRAPR
IL-17R_Hu     RPACFGT-----YVVCYFSEVSCDGDVPDLFGAAPRYPLM-DRFEEVYFRIQ--DLEMFQ
IL-17R_Mu     RPACFGT-----YVVCYFSGICSERDVPDLFNITSRYPLM-DRFEEVYFRIQ--DLEMFE
DCRS10        QGSMNFR-----FIPVLFPNAK-KEHVPTWLQNTHVYSWP-KNKKNILLRLL-REEEYVA
DCRS10_Mu     QGSMNFR-----FIPVLFPNAK-KEHVPTWLQNTHVYSWP-KNKKNILLRLL-REEEYVA
DCRS9_Hu      RPL---------LLLAYFSRLCAKGDIPPPLRALPRYRLL-RDLPRLLRALD--ARPFAE
DCRS8_Hu      QAKQSSSAALSKFIAVYFDYSC-EGDVPGILDLSTKYRLM-DNLPQLCSHLHSRDHGLQE
IL-17R_Ce     HNFPEAR---KKYAVVRFNYSP---HVPPNLAILNLPTFIPEQFAQLTAFLHN-VEHTER
DCRS6_Hu      SQIHLHK-----YVVVYFREID-TKDDYNALSVCPKYHLM-KDATAFCAELL---HVKQQ
DCRS6_Ce      RSVPKEV----EYVLPRDQKLL--EDAFDITIADPLVIDIPIEDVAIPENVP--IHHESC
                                                               .    :

DCRS7_Mu      AGRPADRVER-----VT----QALRSALDSCTS-----------
DCRS7_Hu      SGRLQERAEQ-----VS----RALQPALDSYFHPP---------
IL-17R_Hu     PGRMHRVGELSGDNYLRS---PGGRQLRAALDRFRDWQVRCPDW
IL-17R_Mu     PGRMHHVRELTGDNYLQS---PSGRQLKEAVLRFQEWQTQCPDW
DCRS10        P----PRGPL-----------PTLQVVPL---------------
DCRS10_Mu     P----PRGPL-----------PTLQVVPL---------------
DCRS9_Hu      ATSWGRLGAR-----------QRRQSRLELCSR-----------
DCRS8_Hu      PGQHTRQGSR-----RNYFRSKSGRSLYVAICNMHQFIDEEPDW
IL-17R_Ce     ANVTQNISEA------Q------IHEWNLCASRMMSFFVRNPNW
DCRS6_Hu      VS----AGKR-------------SQACHDGCCSL----------
DCRS6_Ce      DSIDSRNNSK-------------THSTDSGVSSLSS----NS--
                                       :
```

FIG. 1B

SEQUENCE SUBMISSION

SEQ ID NO: 1 is primate DCRS6 nucleotide sequence.
SEQ ID NO: 2 is primate DCRS6 polypeptide sequence.
SEQ ID NO: 3 is primate DCRS6 reverse translation.
SEQ ID NO: 4 is rodent DCRS6 nucleotide sequence.
SEQ ID NO: 5 is rodent DCRS6 polypeptide sequence.
SEQ ID NO: 6 is rodent DCRS6 reverse translation.
SEQ ID NO: 7 is primate DCRS7 nucleotide sequence.
SEQ ID NO: 8 is primate DCRS7 polypeptide sequence.
SEQ ID NO: 9 is primate DCRS7 reverse translation.
SEQ ID NO: 10 is rodent DCRS7 nucleotide sequence.
SEQ ID NO: 11 is rodent DCRS7 polypeptide sequence.
SEQ ID NO: 12 is rodent DCRS7 reverse translation.
SEQ ID NO: 13 is primate DCRS8 nucleotide sequence.
SEQ ID NO: 14 is primate DCRS8 polypeptide sequence.
SEQ ID NO: 15 is primate DCRS8 reverse translation.
SEQ ID NO: 16 is primate DCRS9 nucleotide sequence.
SEQ ID NO: 17 is primate DCRS9 polypeptide sequence.
SEQ ID NO: 18 is primate DCRS9 reverse translation.
SEQ ID NO: 19 is rodent DCRS9 nucleotide sequence.
SEQ ID NO: 20 is rodent DCRS9 polypeptide sequence.
SEQ ID NO: 21 is rodent DCRS9 reverse translation.
SEQ ID NO: 22 is primate DCRS10 nucleotide sequence.
SEQ ID NO: 23 is primate DCRS10 polypeptide sequence.
SEQ ID NO: 24 is primate DCRS10 reverse translation.
SEQ ID NO: 25 is rodent DCRS10 nucleotide sequence.
SEQ ID NO: 26 is rodent DCRS10 polypeptide sequence.
SEQ ID NO: 27 is rodent DCRS10 reverse translation.
SEQ ID NO: 28 is primate IL-17 receptor peptide sequence.
SEQ ID NO: 29 is rodent IL-17 receptor peptide sequence.
SEQ ID NO: 30 is worm IL-17 receptor peptide sequence.
SEQ ID NO: 31 is worm DCRS6 nucleotide sequence.

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<120> Mammalian Receptor Proteins; Related Reagents and Methods

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<222> (46)..(1509)

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                    -10                 -5                  -1   1

gta ccc cga gag ccg acc gtt caa tgt ggc tct gaa act ggg cca tct      96
Val Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser
                5                   10                  15

cca gag tgg atg cta caa cat gat cta atc ccg gga gac ttg agg gac     144
Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp
        20                  25                  30

ctc cga gta gaa cct gtt aca act agt gtt gca aca ggg gac tat tca     192
Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser
    35                  40                  45

att ttg atg aat gta agc tgg gta ctc cgg gca gat gcc agc atc cgc     240
Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg
50                  55                  60                  65

ttg ttg aag gcc acc aag att tgt gtg acg ggc aaa agc aac ttc cag     288
Leu Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln
                70                  75                  80

tcc tac agc tgt gtg agg tgc aat tac aca gag gcc ttc cag act cag     336
Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln
            85                  90                  95

acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tat atc ggc ttc cct     384
Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro
        100                 105                 110

gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat att cct aat     432
Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn
    115                 120                 125

gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat ttc acc tca     480
Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser
130                 135                 140                 145

cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag tgt gtc aag     528
Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys
                150                 155                 160

gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag aag aat gag     576
Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu
            165                 170                 175

gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga aac aga tac     624
Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr
        180                 185                 190
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atg gct ctt atc caa cac agc act atc atc ggg ttt tct cag gtg ttt    672
Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe
    195                 200                 205

gag cca cac cag aag aaa caa acg cga gct tca gtg gtg att cca gtg    720
Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val
210                 215                 220                 225

act ggg gat agt gaa ggt gct acg gtg cag ctg act cca tat ttt cct    768
Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro
                230                 235                 240

act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc    816
Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys
            245                 250                 255

cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa agc aag ccg    864
Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro
        260                 265                 270

gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg    912
Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp
    275                 280                 285

gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa agg atc aag    960
Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys
290                 295                 300                 305

aag act tcc ttt tct acc acc aca cta ctg ccc ccc att aag gtt ctt    1008
Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu
                310                 315                 320

gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att tgt tac ttc    1056
Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe
            325                 330                 335

act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc ctt gaa aag    1104
Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys
        340                 345                 350

tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc    1152
Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala
    355                 360                 365

act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt tcc aat gac    1200
Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp
370                 375                 380                 385

gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc    1248
Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro
                390                 395                 400

agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc    1296
Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys
            405                 410                 415

agt gat cta aga agc cag att cat ctg cac aaa tac gtg gtg gtc tac    1344
Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr
        420                 425                 430
```

```
ttt aga gag att gat aca aaa gac gat tac aat gct ctc agt gtc tgc    1392
Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys
    435                 440                 445

ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt    1440
Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu
450                 455                 460                 465

ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc    1488
Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys
                470                 475                 480

cac gat ggc tgc tgc tcc ttg tagcccaccc atgagaagca agagacctta       1539
His Asp Gly Cys Cys Ser Leu
            485

aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgatcctga agcttactat 1599

gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaatt ttcaaatatt 1659

gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt 1719

tatacataga aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca 1779

ataaagcatc ttcagcc                                                 1796


<210> 2
<211> 502
<212> PRT
<213> Unknown

<400> 2
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
                -10                 -5                  -1   1

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
            5                   10                  15

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
    20                  25                  30

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 35                 40                  45                  50

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
                55                  60                  65

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
            70                  75                  80

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
        85                  90                  95

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
    100                 105                 110

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
115                 120                 125                 130
```

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
135 140 145

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
150 155 160

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
165 170 175

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
180 185 190

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
195 200 205 210

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
215 220 225

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
230 235 240

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
245 250 255

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
260 265 270

Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
275 280 285 290

Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
295 300 305

Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
310 315 320

Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
325 330 335

Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
340 345 350

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
355 360 365 370

Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
375 380 385

Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
390 395 400

Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
405 410 415

Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
420 425 430

Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
435 440 445 450

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
455 460 465

His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
470 475 480

Asp Gly Cys Cys Ser Leu
485

<210> 3
<211> 1506
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(1506)
<223> n may be a, c, g, or t

<400> 3
atgwsnytng tnytnytnws nytngcngcn ytntgymgnw sngcngtncc nmgngarccn 60

acngtncart gyggnwsnga racnggnccn wsnccngart ggatgytnca rcaygayytn 120

athccnggng ayytnmgnga yytnmgngtn garccngtna cnacnwsngt ngcnacnggn 180

gaytaywsna thytnatgaa ygtnwsntgg gtnytnmgng cngaygcnws nathmgnytn 240

ytnaargcna cnaarathtg ygtnacnggn aarwsnaayt tycarwsnta ywsntgygtn 300

mgntgyaayt ayacngargc nttycaracn caracnmgnc cnwsnggngg naartggacn 360

ttywsntaya thggnttycc ngtngarytn aayacngtnt ayttyathgg ngcncayaay 420

athccnaayg cnaayatgaa ygargayggn ccnwsnatgw sngtnaaytt yacnwsnccn 480

ggntgyytng aycayathat gaartayaar aaraartgyg tnaargcngg nwsnytntgg 540

gayccnaaya thacngcntg yaaraaraay gargaracng tngargtnaa yttyacnacn 600

acnccnytng gnaaymgnta yatggcnytn athcarcayw snacnathat hggnttywsn 660

cargtnttyg arccncayca raaraarcar acnmgngcnw sngtngtnat hccngtnacn 720

ggngaywsng arggngcnac ngtncarytn acnccntayt tyccnacntg yggnwsngay 780

tgyathmgnc ayaarggnac ngtngtnytn tgyccncara cnggngtncc nttyccnytn 840

gayaayaaya arwsnaarcc nggnggntgg ytnccnytny tnytnytnws nytnytngtn 900

gcnacntggg tnytngtngc nggnathtay ytnatgtggm gncaygarmg nathaaraar 960

acnwsnttyw snacnacnac nytnytnccn ccnathaarg tnytngtngt ntayccnwsn 1020

garathtgyt tycaycayac nathtgytay ttyacngart tyytncaraa ycaytgymgn 1080

wsngargtna thytngaraa rtggcaraar aaraarathg cngaratggg nccngtncar 1140

tggytngcna cncaraaraa rgcngcngay aargtngtnt tyytnytnws naaygaygtn 1200

aaywsngtnt gygayggnac ntgyggnaar wsngarggnw snccnwsnga raaywsncar 1260

gayytnttyc cnytngcntt yaayytntty tgywsngayy tnmgnwsnca rathcayytn 1320

cayaartayg tngtngtnta yttymgngar athgayacna argaygayta yaaygcnytn 1380

wsngtntgyc cnaartayca yytnatgaar gaygcnacng cnttytgygc ngarytnytn 1440

caygtnaarc arcargtnws ngcnggnaar mgnwsncarg cntgycayga yggntgytgy 1500

wsnytn 1506

<210> 4
<211> 637
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:rodent; surmised
      Mus musculus .

<220>
<221> CDS
<222> (1)..(210)

<400> 4
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gat ttc agc agc cag acg cat ctg cac aaa tac ctg gag gtc tat ctt    48
Asp Phe Ser Ser Gln Thr His Leu His Lys Tyr Leu Glu Val Tyr Leu
  1               5                  10                  15

ggg gga gca gac ctc aaa ggc gac tat aat gcc ctg agt gtc tgc ccc    96
Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
             20                  25                  30

caa tat cat ctc atg aag gac gcc aca gct ttc cac aca gaa ctt ctc   144
Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
         35                  40                  45

aag gct acg cag agc atg tca gtg aag aaa cgc tca caa gcc tgc cat   192
Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
     50                  55                  60

gat agc tgt tca ccc ttg tagtccaccc gggggaatag agactctgaa          240
Asp Ser Cys Ser Pro Leu
 65                  70
```

gccttcctac tctcccttcc agtgacaaat gctgtgtgac gactctgaaa tgtgtgggag 300

aggctgtgtg gaggtagtgc tatgtacaaa cttgctttaa aactggagtt tgcaaagtca 360

acctgagcat acacgcctga ggctagtcat tggctggatt tatgaagaca acacagttac 420

agacaataat gagtgggacc tacatttggg atataccca agctgggtaa tgattatcac 480

tgagaaccac gcactctggc catgaggtaa tacggcactt ccctgtcagg ctgtctgtca 540

ggttgggtct gtcttgcact gcccatgctc tatgctgcac gtagaccgtt ttgtaacatt 600

ttaatctgtt aatgaataat ccgtttggga ggctctc 637

<210> 5
<211> 70
<212> PRT
<213> Unknown

<400> 5
Asp Phe Ser Ser Gln Thr His Leu His Lys Tyr Leu Glu Val Tyr Leu
1 5 10 15

Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
20 25 30

Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
35 40 45

Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
50 55 60

Asp Ser Cys Ser Pro Leu
65 70

<210> 6
<211> 210
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(210)
<223> n may be a, c, g, or t

<400> 6
gayttywsnw sncaracnca yytncayaar tayytngarg tntayytngg nggngcngay 60

ytnaarggng aytayaaygc nytnwsngtn tgyccncart aycayytnat gaargaygcn 120

acngcnttyc ayacngaryt nytnaargcn acncarwsna tgwsngtnaa raarmgnwsn 180

cargcntgyc aygaywsntg ywsnccnytn 210

<210> 7
<211> 2308
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>
<221> CDS
<222> (181)..(2289)

<220>

<221> mat_peptide
<222> (241)..(2289)

<220>
<221> misc_feature
<222> (664)
<223> Xaa translation depends on genetic code

<400> 7
gagtcaggac tcccaggaca gagagtgcac aaactaccca gcacagcccc ctccgccccc 60

tctggaggct gaagagggat tccagcccct gccacccaca gacacgggct gactggggtg 120

tctgcccccc ttgggggcan ccacagggcc tcaggcctgg gtgccacctg gcactagaag 180

atg cct gtg ccc tgg ttc ttg ctg tcc ttg gca ctg ggc cga agc cag 228
Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
-20 -15 -10 -5

tgg atc ctt tct ctg gag agg ctt gtg ggg cct cag gac gct acc cac 276
Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
-1 1 5 10

tgc tct ccg ggc ctc tcc tgc cgc ctc tgg gac agt gac ata ctc tgc 324
Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
15 20 25

ctg cct ggg gac atc gtg cct gct ccg ggc ccc gtg ctg gcg cct acg 372
Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
30 35 40

cac ctg cag aca gag ctg gtg ctg agg tgc cag aag gag acc gac tgt 420
His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
45 50 55 60

gac ctc tgt ctg cgt gtg gct gtc cac ttg gcc gtg cat ggg cac tgg 468
Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
65 70 75

gaa gag cct gaa gat gag gaa aag ttt gga gga gca gct gac tta ggg 516
Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
80 85 90

gtg gag gag cct agg aat gcc tct ctc cag gcc caa gtc gtg ctc tcc 564
Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
95 100 105

ttc cag gcc tac cct act gcc cgc tgc gtc ctg ctg gag gtg caa gtg 612
Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
110 115 120

cct gct gcc ctt gtg cag ttt ggt cag tct gtg ggc tct gtg gta tat 660
Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
125 130 135 140

gac tgc ttc gag gct gcc cta ggg agt gag gta cga atc tgg tcc tat 708
Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
145 150 155

act cag ccc agg tac gag aag gaa ctc aac cac aca cag cag ctg cct 756

```
Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
            160                 165                 170

gac tgc agg ggg ctc gaa gtc tgg aac agc atc ccg agc tgc tgg gcc    804
Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala
        175                 180                 185

ctg ccc tgg ctc aac gtg tca gca gat ggt gac aac gtg cat ctg gtt    852
Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val
    190                 195                 200

ctg aat gtc tct gag gag cag cac ttc ggc ctc tcc ctg tac tgg aat    900
Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn
205                 210                 215                 220

cag gtc cag ggc ccc cca aaa ccc cgg tgg cac aaa aac ctg act gga    948
Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly
                225                 230                 235

ccg cag atc att acc ttg aac cac aca gac ctg gtt ccc tgc ctc tgt    996
Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys
            240                 245                 250

att cag gtg tgg cct ctg gaa cct gac tcc gtt agg acg aac atc tgc    1044
Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys
        255                 260                 265

ccc ttc agg gag gac ccc cgc gca cac cag aac ctc tgg caa gcc gcc    1092
Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala
    270                 275                 280

cga ctg cga ctg ctg acc ctg cag agc tgg ctg ctg gac gca ccg tgc    1140
Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys
285                 290                 295                 300

tcg ctg ccc gca gaa gcg gca ctg tgc tgg cgg gct ccg ggt ggg gac    1188
Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp
                305                 310                 315

ccc tgc cag cca ctg gtc cca ccg ctt tcc tgg gag aat gtc act gtg    1236
Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr Val
            320                 325                 330

gac gtg aac agc tcg gag aag ctg cag ctg cag gag tgc ttg tgg gct    1284
Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala
        335                 340                 345

gac tcc ctg ggg cct ctc aaa gac gat gtg cta ctg ttg gag aca cga    1332
Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg
    350                 355                 360

ggc ccc cag gac aac aga tcc ctc tgt gcc ttg gaa ccc agt ggc tgt    1380
Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys
365                 370                 375                 380

act tca cta ccc agc aaa gcc tcc acg agg gca gct cgc ctt gga gag    1428
Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu
                385                 390                 395

tac tta cta caa gac ctg cag tca ggc cag tgt ctg cag cta tgg gac    1476
```

Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp
400 405 410

gat gac ttg gga gcg cta tgg gcc tgc ccc atg gac aaa tac atc cac 1524
Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His
415 420 425

aag cgc tgg gcc ctc gtg tgg ctg gcc tgc cta ctc ttt gcc gct gcg 1572
Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala
430 435 440

ctt tcc ctc atc ctc ctt ctc aaa aag gat cac gcg aaa ggg tgg ctg 1620
Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu
445 450 455 460

agg ctc ttg aaa cag gac gtc cgc tcg ggg gcg gcc gcc agg ggc cgc 1668
Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg Gly Arg
465 470 475

gcg gct ctg ctc ctc tac tca gcc gat gac tcg ggt ttc gag cgc ctg 1716
Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu
480 485 490

gtg ggc gcc ctg gcg tcg gcc ctg tgc cag ctg ccg ctg cgc gtg gcc 1764
Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala
495 500 505

gta gac ctg tgg agc cgt cgt gaa ctg agc gcg cag ggg ccc gtg gct 1812
Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala
510 515 520

tgg ttt cac gcg cag cgg cgc cag acc ctg cag gag ggc ggc gtg gtg 1860
Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val
525 530 535 540

gtc ttg ctc ttc tct ccc ggt gcg gtg gcg ctg tgc agc gag tgg cta 1908
Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu
545 550 555

cag gat ggg gtg tcc ggg ccc ggg gcg cac ggc ccg cac gac gcc ttc 1956
Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe
560 565 570

cgc gcc tcg ctc agc tgc gtg ctg ccc gac ttc ttg cag ggc cgg gcg 2004
Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala
575 580 585

ccc ggc agc tac gtg ggg gcc tgc ttc gac agg ctg ctc cac ccg gac 2052
Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp
590 595 600

gcc gta ccc gcc ctt ttc cgc acc gtg ccc gtc ttc aca ctg ccc tcc 2100
Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser
605 610 615 620

caa ctg cca gac ttc ctg ggg gcc ctg cag cag cct cgc gcc ccg cgt 2148
Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg
625 630 635

tcc ggg cgg ctc caa gag aga gcg gag caa gtg tcc cgg gcc ctt cag 2196

```
Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
            640                 645                 650

cca gcc ctg gat agc tac ttc cat ccc ccg ggg acn tcc gcg ccg gga    2244
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly
        655                 660                 665

cgc ggg gtg gga cca ggg gcg gga cct ggg gcg ggg gac ggg act        2289
Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr
    670                 675                 680

taaataaagg cagacgctg                                               2308


<210> 8
<211> 703
<212> PRT
<213> Unknown

<400> 8
Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
-20                 -15                 -10                 -5

Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
            -1  1               5                   10

Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
        15                  20                  25

Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
    30                  35                  40

His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
 45                  50                  55                  60

Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
                65                  70                  75

Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
            80                  85                  90

Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
        95                  100                 105

Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
    110                 115                 120

Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
125                 130                 135                 140

Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
                145                 150                 155

Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
            160                 165                 170

Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala
        175                 180                 185

Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val
```

190 195 200

Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn
205 210 215 220

Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly
225 230 235

Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys
240 245 250

Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys
255 260 265

Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala
270 275 280

Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys
285 290 295 300

Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp
305 310 315

Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr Val
320 325 330

Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala
335 340 345

Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg
350 355 360

Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys
365 370 375 380

Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu
385 390 395

Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp
400 405 410

Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His
415 420 425

Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala
430 435 440

Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu
445 450 455 460

Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg Gly Arg
465 470 475

Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu
480 485 490

Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala
495 500 505

Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala

```
    510                 515                 520

Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val
525                 530                 535                 540

Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu
                545                 550                 555

Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe
            560                 565                 570

Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala
        575                 580                 585

Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp
    590                 595                 600

Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser
605                 610                 615                 620

Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg
                625                 630                 635

Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
            640                 645                 650

Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly
        655                 660                 665

Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr
    670                 675                 680


<210> 9
<211> 2109
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(2109)
<223> n may be a, c, g, or t

<400> 9
atgccngtnc cntggttyyt nytnwsnytn gcnytnggnm gnwsncartg gathytnwsn 60

ytngarmgny tngtnggncc ncargaygcn acncaytgyw snccnggnyt nwsntgymgn 120

ytntgggayw sngayathyt ntgyytnccn ggngayathg tnccngcncc nggnccngtn 180

ytngcnccna cncayytnca racngarytn gtnytnmgnt gycaraarga racngaytgy 240

gayytntgyy tnmgngtngc ngtncayytn gcngtncayg gncaytggga rgarccngar 300

gaygargara arttyggngg ngcngcngay ytnggngtng argarccnmg naaygcnwsn 360

ytncargcnc argtngtnyt nwsnttycar gcntayccna cngcnmgntg ygtnytnytn 420

gargtncarg tnccngcngc nytngtncar ttyggncarw sngtnggnws ngtngtntay 480
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gaytgyttyg argcngcnyt nggnwsngar gtnmgnatht ggwsntayac ncarccnmgn 540
taygaraarg arytnaayca yacncarcar ytnccngayt gymgnggnyt ngargtntgg 600
aaywsnathc cnwsntgytg ggcnytnccn tggytnaayg tnwsngcnga yggngayaay 660
gtncayytng tnytnaaygt nwsngargar carcayttyg gnytnwsnyt ntaytggaay 720
cargtncarg gnccnccnaa rccnmgntgg cayaaraayy tnacnggncc ncarathath 780
acnytnaayc ayacngayyt ngtnccntgy ytntgyathc argtntggcc nytngarccn 840
gaywsngtnm gnacnaayat htgyccntty mgngargayc cnmgngcnca ycaraayytn 900
tggcargcng cnmgnytnmg nytnytnacn ytncarwsnt ggytnytnga ygcnccntgy 960
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carytncarg artgyytntg ggcngaywsn ytnggnccny tnaargayga ygtnytnytn 1140
ytngaracnm gnggnccnca rgayaaymgn wsnytntgyg cnytngarcc nwsnggntgy 1200
acnwsnytnc cnwsnaargc nwsnacnmgn gcngcnmgny tnggngarta yytnytncar 1260
gayytncarw snggncartg yytncarytn tgggaygayg ayytnggngc nytntgggcn 1320
tgyccnatgg ayaartayat hcayaarmgn tgggcnytng tntggytngc ntgyytnytn 1380
ttygcngcng cnytnwsnyt nathytnytn ytnaaraarg aycaygcnaa rggntggytn 1440
mgnytnytna arcargaygt nmgnwsnggn gcngcngcnm gnggnmgngc ngcnytnytn 1500
ytntaywsng cngaygayws nggnttygar mgnytngtng gngcnytngc nwsngcnytn 1560
tgycarytnc cnytnmgngt ngcngtngay ytntggwsnm gnmgngaryt nwsngcncar 1620
ggnccngtng cntggttyca ygcncarmgn mgncaracny tncargargg nggngtngtn 1680
gtnytnytnt tywsnccngg ngcngtngcn ytntgywsng artggytnca rgayggngtn 1740
wsnggnccng gngcncaygg nccncaygay gcnttymgng cnwsnytnws ntgygtnytn 1800
ccngayttyy tncarggnmg ngcnccnggn wsntaygtng gngcntgytt ygaymgnytn 1860
ytncayccng aygcngtncc ngcnytntty mgnacngtnc cngtnttyac nytnccnwsn 1920
carytnccng ayttyytngg ngcnytncar carccnmgng cnccnmgnws nggnmgnytn 1980
cargarmgng cngarcargt nwsnmgngcn ytncarccng cnytngayws ntayttycay 2040
ccnccnggna cnwsngcncc nggnmgnggn gtnggnccng gngcnggncc nggngcnggn 2100
gayggnacn 2109

<210> 10
<211> 2314
<212> DNA

<213> Unknown

<220>
<223> Description of Unknown Organism:rodent; surmised Mus musculus

<220>
<221> CDS
<222> (199)..(2292)

<220>
<221> mat_peptide
<222> (259)..(2292)

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agcatggctg gagaggaatt ctagcccttg ctctctccca gggacacggg gctgattgtc 120

agcaggggcg aggggtctgc cccccttgg gggggcagga cggggcctca ggcctgggtg 180

ctgtccggca cctggaag atg cct gtg tcc tgg ttc ctg ctg tcc ttg gca 231
Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala
-20 -15 -10

ctg ggc cga aac cct gtg gtc gtc tct ctg gag aga ctg atg gag cct 279
Leu Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro
-5 -1 1 5

cag gac act gca cgc tgc tct cta ggc ctc tcc tgc cac ctc tgg gat 327
Gln Asp Thr Ala Arg Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp
10 15 20

ggt gac gtg ctc tgc ctg cct gga agc ctc cag tct gcc cca ggc cct 375
Gly Asp Val Leu Cys Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro
25 30 35

gtg cta gtg cct acc cgc ctg cag acg gag ctg gtg ctg agg tgt cca 423
Val Leu Val Pro Thr Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro
40 45 50 55

cag aag aca gat tgc gcc ctc tgt gtc cgt gtg gtg gtc cac ttg gcc 471
Gln Lys Thr Asp Cys Ala Leu Cys Val Arg Val Val Val His Leu Ala
60 65 70

gtg cat ggg cac tgg gca gag cct gaa gaa gct gga aag tct gat tca 519
Val His Gly His Trp Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser
75 80 85

gaa ctc cag gag tct agg aac gcc tct ctc cag gcc cag gtg gtg ctc 567
Glu Leu Gln Glu Ser Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu
90 95 100

tcc ttc cag gcc tac ccc atc gcc cgc tgt gcc ctg ctg gag gtc cag 615
Ser Phe Gln Ala Tyr Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln
105 110 115

gtg ccc gct gac ctg gtg cag cct ggt cag tcc gtg ggt tct gcg gta 663
Val Pro Ala Asp Leu Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val
120 125 130 135

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ttt gac tgt ttc gag gct agt ctt ggg gct gag gta cag atc tgg tcc    711
Phe Asp Cys Phe Glu Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser
                140                 145                 150

tac acg aag ccc agg tac cag aaa gag ctc aac ctc aca cag cag ctg    759
Tyr Thr Lys Pro Arg Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu
            155                 160                 165

cct gac tgc agg ggt ctt gaa gtc cgg gac agc atc cag agc tgc tgg    807
Pro Asp Cys Arg Gly Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp
        170                 175                 180

gtc ctg ccc tgg ctc aat gtg tct aca gat ggt gac aat gtc ctt ctg    855
Val Leu Pro Trp Leu Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu
    185                 190                 195

aca ctg gat gtc tct gag gag cag gac ttt agc ttc tta ctg tac ctg    903
Thr Leu Asp Val Ser Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu
200                 205                 210                 215

cgt cca gtc ccg gat gct ctc aaa tcc ttg tgg tac aaa aac ctg act    951
Arg Pro Val Pro Asp Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr
                220                 225                 230

gga cct cag aac att act tta aac cac aca gac ctg gtt ccc tgc ctc    999
Gly Pro Gln Asn Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu
            235                 240                 245

tgc att cag gtg tgg tcg cta gag cca gac tct gag agg gtc gaa ttc    1047
Cys Ile Gln Val Trp Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe
        250                 255                 260

tgc ccc ttc cgg gaa gat ccc ggt gca cac agg aac ctc tgg cac ata    1095
Cys Pro Phe Arg Glu Asp Pro Gly Ala His Arg Asn Leu Trp His Ile
    265                 270                 275

gcc agg ctg cgg gta ctg tcc cca ggg gta tgg cag cta gat gcg cct    1143
Ala Arg Leu Arg Val Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro
280                 285                 290                 295

tgc tgt ctg ccg ggc aag gta aca ctg tgc tgg cag gca cca gac cag    1191
Cys Cys Leu Pro Gly Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln
                300                 305                 310

agt ccc tgc cag cca ctt gtg cca cca gtg ccc cag aag aac gcc act    1239
Ser Pro Cys Gln Pro Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr
            315                 320                 325

gtg aat gag cca caa gat ttc cag ttg gtg gca ggc cac ccc aac ctc    1287
Val Asn Glu Pro Gln Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu
        330                 335                 340

tgt gtc cag gtg agc acc tgg gag aag gtt cag ctg caa gcg tgc ttg    1335
Cys Val Gln Val Ser Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Leu
    345                 350                 355

tgg gct gac tcc ttg ggg ccc ttc aag gat gat atg ctg tta gtg gag    1383
Trp Ala Asp Ser Leu Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu
360                 365                 370                 375
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atg aaa acc ggc ctc aac aac aca tca gtc tgt gcc ttg gaa ccc agt 1431
Met Lys Thr Gly Leu Asn Asn Thr Ser Val Cys Ala Leu Glu Pro Ser
380 385 390

ggc tgt aca cca ctg ccc agc atg gcc tcc acg aga gct gct cgc ctg 1479
Gly Cys Thr Pro Leu Pro Ser Met Ala Ser Thr Arg Ala Ala Arg Leu
395 400 405

gga gag gag ttg ctg caa gac ttc cga tca cac cag tgt atg cag ctg 1527
Gly Glu Glu Leu Leu Gln Asp Phe Arg Ser His Gln Cys Met Gln Leu
410 415 420

tgg aac gat gac aac atg gga tcg cta tgg gcc tgc ccc atg gac aag 1575
Trp Asn Asp Asp Asn Met Gly Ser Leu Trp Ala Cys Pro Met Asp Lys
425 430 435

tac atc cac agg cgc tgg gtc cta gta tgg ctg gcc tgc cta ctc ttg 1623
Tyr Ile His Arg Arg Trp Val Leu Val Trp Leu Ala Cys Leu Leu Leu
440 445 450 455

gct gcg gcg ctt ttc ttc ttc ctc ctt cta aaa aag gac cgc agg aaa 1671
Ala Ala Ala Leu Phe Phe Phe Leu Leu Leu Lys Lys Asp Arg Arg Lys
460 465 470

gcg gcc cgt ggc tcc cgc acg gcc ttg ctc ctc cac tcc gcc gac gga 1719
Ala Ala Arg Gly Ser Arg Thr Ala Leu Leu Leu His Ser Ala Asp Gly
475 480 485

gcg ggc tac gag cgc ctg gtg gga gca ctg gcg tcc gcg ttg agc cag 1767
Ala Gly Tyr Glu Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Ser Gln
490 495 500

atg cca ctg cgc gtg gcc gtg gac ctg tgg agc cgc cgc gag ctg agc 1815
Met Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser
505 510 515

gcg cac gga gcc cta gcc tgg ttc cac cac cag cga cgc cgt atc ctg 1863
Ala His Gly Ala Leu Ala Trp Phe His His Gln Arg Arg Arg Ile Leu
520 525 530 535

cag gag ggt ggc gtg gta atc ctt ctc ttc tcg ccc gcg gcc gtg gcg 1911
Gln Glu Gly Gly Val Val Ile Leu Leu Phe Ser Pro Ala Ala Val Ala
540 545 550

cag tgt cag cag tgg ctg cag ctc cag aca gtg gag ccc ggg ccg cat 1959
Gln Cys Gln Gln Trp Leu Gln Leu Gln Thr Val Glu Pro Gly Pro His
555 560 565

gac gcc ctc gcc gcc tgg ctc agc tgc gtg cta ccc gat ttc ctg caa 2007
Asp Ala Leu Ala Ala Trp Leu Ser Cys Val Leu Pro Asp Phe Leu Gln
570 575 580

ggc cgg gcg acc ggc cgc tac gtc ggg gtc tac ttc gac ggg ctg ctg 2055
Gly Arg Ala Thr Gly Arg Tyr Val Gly Val Tyr Phe Asp Gly Leu Leu
585 590 595

cac cca gac tct gtg ccc tcc ccg ttc cgc gtc gcc ccg ctc ttc tcc 2103
His Pro Asp Ser Val Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser
600 605 610 615

ctg ccc tcg cag ctg ccg gct ttc ctg gat gca ctg cag gga ggc tgc 2151
Leu Pro Ser Gln Leu Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys
620 625 630

tcc act tcc gcg ggg cga ccc gcg gac cgg gtg gaa cga gtg acc cag 2199
Ser Thr Ser Ala Gly Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln
635 640 645

gcg ctg cgg tcc gcc ctg gac agc tgt act tct agc tcg gaa gcc cca 2247
Ala Leu Arg Ser Ala Leu Asp Ser Cys Thr Ser Ser Ser Glu Ala Pro
650 655 660

ggc tgc tgc gag gaa tgg gac ctg gga ccc tgc act aca cta gaa 2292
Gly Cys Cys Glu Glu Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
665 670 675

taaaagccga tacagtattc ct 2314

<210> 11
<211> 698
<212> PRT
<213> Unknown

<400> 11
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-20 -15 -10 -5

Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln Asp Thr Ala Arg
-1 1 5 10

Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp Gly Asp Val Leu Cys
15 20 25

Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val Leu Val Pro Thr
30 35 40

Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln Lys Thr Asp Cys
45 50 55 60

Ala Leu Cys Val Arg Val Val Val His Leu Ala Val His Gly His Trp
65 70 75

Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu Leu Gln Glu Ser
80 85 90

Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser Phe Gln Ala Tyr
95 100 105

Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln Val Pro Ala Asp Leu
110 115 120

Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val Phe Asp Cys Phe Glu
125 130 135 140

Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser Tyr Thr Lys Pro Arg
145 150 155

Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu Pro Asp Cys Arg Gly

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            160                 165                 170

Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp Val Leu Pro Trp Leu
        175                 180                 185

Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu Thr Leu Asp Val Ser
    190                 195                 200

Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu Arg Pro Val Pro Asp
205                 210                 215                 220

Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr Gly Pro Gln Asn Ile
                225                 230                 235

Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys Ile Gln Val Trp
            240                 245                 250

Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe Cys Pro Phe Arg Glu
        255                 260                 265

Asp Pro Gly Ala His Arg Asn Leu Trp His Ile Ala Arg Leu Arg Val
    270                 275                 280

Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro Cys Cys Leu Pro Gly
285                 290                 295                 300

Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln Ser Pro Cys Gln Pro
                305                 310                 315

Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr Val Asn Glu Pro Gln
            320                 325                 330

Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu Cys Val Gln Val Ser
        335                 340                 345

Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Leu Trp Ala Asp Ser Leu
    350                 355                 360

Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu Met Lys Thr Gly Leu
365                 370                 375                 380

Asn Asn Thr Ser Val Cys Ala Leu Glu Pro Ser Gly Cys Thr Pro Leu
                385                 390                 395

Pro Ser Met Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu Glu Leu Leu
            400                 405                 410

Gln Asp Phe Arg Ser His Gln Cys Met Gln Leu Trp Asn Asp Asp Asn
        415                 420                 425

Met Gly Ser Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His Arg Arg
    430                 435                 440

Trp Val Leu Val Trp Leu Ala Cys Leu Leu Leu Ala Ala Ala Leu Phe
445                 450                 455                 460

Phe Phe Leu Leu Leu Lys Lys Asp Arg Arg Lys Ala Ala Arg Gly Ser
                465                 470                 475

Arg Thr Ala Leu Leu Leu His Ser Ala Asp Gly Ala Gly Tyr Glu Arg
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480 485 490

Leu Val Gly Ala Leu Ala Ser Ala Leu Ser Gln Met Pro Leu Arg Val
495 500 505

Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala His Gly Ala Leu
510 515 520

Ala Trp Phe His His Gln Arg Arg Arg Ile Leu Gln Glu Gly Gly Val
525 530 535 540

Val Ile Leu Leu Phe Ser Pro Ala Ala Val Ala Gln Cys Gln Gln Trp
545 550 555

Leu Gln Leu Gln Thr Val Glu Pro Gly Pro His Asp Ala Leu Ala Ala
560 565 570

Trp Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala Thr Gly
575 580 585

Arg Tyr Val Gly Val Tyr Phe Asp Gly Leu Leu His Pro Asp Ser Val
590 595 600

Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser Leu Pro Ser Gln Leu
605 610 615 620

Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys Ser Thr Ser Ala Gly
625 630 635

Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln Ala Leu Arg Ser Ala
640 645 650

Leu Asp Ser Cys Thr Ser Ser Ser Glu Ala Pro Gly Cys Cys Glu Glu
655 660 665

Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
670 675

<210> 12
<211> 2094
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(2094)
<223> n may be a, c, g, or t

<400> 12
atgccngtnw sntggttyyt nytnwsnytn gcnytnggnm gnaayccngt ngtngtnwsn 60

ytngarmgny tnatggarcc ncargayacn gcnmgntgyw snytnggnyt nwsntgycay 120

ytntgggayg gngaygtnyt ntgyytnccn ggnwsnytnc arwsngcncc nggnccngtn 180

ytngtnccna cnmgnytnca racngarytn gtnytnmgnt gyccncaraa racngaytgy 240

gcnytntgyg tnmgngtngt ngtncayytn gcngtncayg gncaytgggc ngarccngar 300

gargcnggna arwsngayws ngarytncar garwsnmgna aygcnwsnyt ncargcncar 360
gtngtnytnw snttycargc ntayccnath gcnmgntgyg cnytnytnga rgtncargtn 420
ccngcngayy tngtncarcc nggncarwsn gtnggnwsng cngtnttyga ytgyttygar 480
gcnwsnytng gngcngargt ncarathtgg wsntayacna arccnmgnta ycaraargar 540
ytnaayytha cncarcaryt nccngaytgy mgnggnytng argtnmgnga ywsnathcar 600
wsntgytggg tnytnccntg gytnaaygtn wsnacngayg gngayaaygt nytnytnacn 660
ytngaygtnw sngargarca rgayttywsn ttyytnytnt ayytnmgncc ngtnccngay 720
gcnytnaarw snytntggta yaaraayytn acnggnccnc araayathac nytnaaycay 780
acngayytng tnccntgyyt ntgyathcar gtntggwsny tngarccnga ywsngarmgn 840
gtngarttyt gyccnttymg ngargayccn ggngcncaym gnaayytntg gcayathgcn 900
mgnytnmgng tnytnwsncc nggngtntgg carytngayg cnccntgytg yytnccnggn 960
aargtnacny tntgytggca rgcnccngay carwsnccnt gycarccnyt ngtnccnccn 1020
gtnccncara araaygcnac ngtnaaygar ccncargayt tycarytngt ngcnggncay 1080
ccnaayytnt gygtncargt nwsnacntgg garaargtnc arytncargc ntgyytntgg 1140
gcngaywsny tnggnccntt yaargaygay atgytnytng tngaratgaa racnggnytn 1200
aayaayacnw sngtntgygc nytngarccn wsnggntgya cnccnytncc nwsnatggcn 1260
wsnacnmgng cngcnmgnyt nggngargar ytnytncarg ayttymgnws ncaycartgy 1320
atgcarytnt ggaaygayga yaayatgggn wsnytntggg cntgyccnat ggayaartay 1380
athcaymgnm gntgggtnyt ngtntggytn gcntgyytny tnytngcngc ngcnytntty 1440
ttyttyytny tnytnaaraa rgaymgnmgn aargcngcnm gnggnwsnmg nacngcnytn 1500
ytnytncayw sngcngaygg ngcnggntay garmgnytng tnggngcnyt ngcnwsngcn 1560
ytnwsncara tgccnytnmg ngtngcngtn gayytntggw snmgnmgnga rytnwsngcn 1620
cayggngcny tngcntggtt ycaycaycar mgnmgnmgna thytncarga rggnggngtn 1680
gtnathytny tnttywsncc ngcngcngtn gcncartgyc arcartggyt ncarytncar 1740
acngtngarc cnggnccnca ygaygcnytn gcngcntggy tnwsntgygt nytnccngay 1800
ttyytncarg gnmgngcnac nggnmgntay gtnggngtnt ayttygaygg nytnytncay 1860
ccngaywsng tnccnwsncc nttymgngtn gcnccnytnt tywsnytncc nwsncarytn 1920
ccngcnttyy tngaygcnyt ncarggnggn tgywsnacnw sngcnggnmg nccngcngay 1980
mgngtngarm gngtnacnca rgcnytnmgn wsngcnytng aywsntgyac nwsnwsnwsn 2040
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<210> 13
<211> 2786
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
      Homo sapiens

<220>
<221> CDS
<222> (70)..(2283)

<220>
<221> mat_peptide
<222> (118)..(2283)

<220>
<221> misc_feature
<222> (9)..(134)
<223> Xaa translation (9, 18,26, 109,120, 134) depends
      on genetic code

<400> 13
cccacgcntc cgggccagca gcgggcggcc ggggcgcaga gaacggcctg gctgggcgag 60

cgcacggcc atg gcc ccg tgg ctg cag ctc tgc tcc gtc ttc ttt acg gtc 111
          Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val
              -15                 -10                  -5

aac gcc tgc ctc aac ggc tcg cag ctg gct gtn gcc gct ggc ggg tcc   159
Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Xaa Ala Ala Gly Gly Ser
     -1   1               5                  10

ggc cgc gcg cng ggc gcc gac acc tgt agc tgg ang gga gtg ggg cca   207
Gly Arg Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro
 15                  20                  25                  30

gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa tat gac aat   255
Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn
                 35                  40                  45

tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att gct gac gcc   303
Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala
             50                  55                  60

cag aat atc acc atc agc cag tat gct tgc cat gac caa gtg gca gtc   351
Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val
         65                  70                  75

acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc ctg aaa gga   399
Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly
     80                  85                  90

ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga cag ngc caa   447
Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln
 95                 100                 105                 110

caa ctg att cta aag gat ccg aag cag ntc aac agt agc ttc aaa aga   495
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Gln Leu Ile Leu Lys Asp Pro Lys Gln Xaa Asn Ser Ser Phe Lys Arg
                115                 120                 125

act gga atg gaa tct caa cct ttn ctg aat atg aaa ttt gaa acg gat     543
Thr Gly Met Glu Ser Gln Pro Xaa Leu Asn Met Lys Phe Glu Thr Asp
            130                 135                 140

tat ttc gta agg ttg tcc ttt tcc ttc att aaa aac gaa agc aat tac     591
Tyr Phe Val Arg Leu Ser Phe Ser Phe Ile Lys Asn Glu Ser Asn Tyr
        145                 150                 155

cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg ttg tta cag ccg     639
His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro
    160                 165                 170

gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg aac ctg aac atc     687
Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile
175                 180                 185                 190

agc cag cat ggc tcg gac atg cag gtg tcc ttc gac cac gca ccg cac     735
Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His
                195                 200                 205

aac ttc ggc ttc cgt ttc ttc tat ctt cac tac aag ctc aag cac gaa     783
Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu
            210                 215                 220

gga cct ttc aag cga aag acc tgt aag cag gag caa act aca gag atg     831
Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met
        225                 230                 235

acc agc tgc ctc ctt caa aat gtt tct cca ggg gat tat ata att gag     879
Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu
    240                 245                 250

ctg gtg gat gac act aac aca aca aga aaa gtg atg cat tat gcc tta     927
Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu
255                 260                 265                 270

aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga gcc gtg gcc atc     975
Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile
                275                 280                 285

aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg ctc ttc act gtg    1023
Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val
            290                 295                 300

atg tgc cgc aag aag caa caa gaa aat ata tat tca cat tta gat gaa    1071
Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu
        305                 310                 315

gag agc tct gag tct tcc aca tac act gca gca ctc cca aga gag agg    1119
Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg
    320                 325                 330

ctc cgg ccg cgg ccg aag gtc ttt ctc tgc tat tcc agt aaa gat ggc    1167
Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly
335                 340                 345                 350

cag aat cac atg aat gtc gtc cag tgt ttc gcc tac ttc ctc cag gac    1215
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Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp
                355                 360                 365

ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa gac ttc agc ctc     1263
Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu
            370                 375                 380

tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag atc cac gag tcc     1311
Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser
        385                 390                 395

cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag tac ttt gtg gac     1359
Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp
    400                 405                 410

aag aag aac tac aaa cac aaa gga ggt ggc cga ggc tcg ggg aaa gga     1407
Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly
415                 420                 425                 430

gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa aag ctc cgc cag     1455
Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln
                435                 440                 445

gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt atc gcc gtc tac     1503
Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr
            450                 455                 460

ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc cta gac ctg agt     1551
Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser
        465                 470                 475

acc aag tac aga ctc atg gac aat ctt cct cag ctc tgt tcc cac ctg     1599
Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu
    480                 485                 490

cac tcc cga gac cac ggc ctc cag gag ccg ggg cag cac acg cga cag     1647
His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln
495                 500                 505                 510

ggc agc aga agg aac tac ttc cgg agc aag tca ggc cgg tcc cta tac     1695
Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr
                515                 520                 525

gtc gcc att tgc aac atg cac cag ttt att gac gag gag ccc gac tgg     1743
Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp
            530                 535                 540

ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca ctg cgc tac cgg     1791
Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg
        545                 550                 555

gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt tta aat gat gtc     1839
Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val
    560                 565                 570

atg tgc aaa cca ggg cct gag agt gac ttc tgc cta aag gta gag gcg     1887
Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala
575                 580                 585                 590

gct gtt ctt ggg gca acc gga cca gcc gac tcc cag cac gag agt cag     1935
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Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln
                595                 600                 605

cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct gcc ctt gac ggt    1983
His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly
            610                 615                 620

agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa gcc ggc agc ccc    2031
Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro
        625                 630                 635

tcg gac atg ccg cgg gac tca ggc atc tat gac tcg tct gtg ccc tca    2079
Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser
    640                 645                 650

tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg acg gac cag aca    2127
Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr
655                 660                 665                 670

gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct tca ggc ctg ggt    2175
Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly
                675                 680                 685

gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc tct tct ggg tca    2223
Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser
            690                 695                 700

tgc aaa gca gat ctt ggt tgc cgc agc tac act gat gaa ctc cac gcg    2271
Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala
        705                 710                 715

gtc gcc cct ttg taacaaaacg aaagagtcta agcattgcca ctttagctgc        2323
Val Ala Pro Leu
    720

tgcctccctc tgattcccca gctcatctcc ctggttgcat ggcccacttg gagctgaggt 2383

ctcatacaag gatatttgga gtgaaatgct ggccagtact tgttctccct tgccccaacc 2443

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catgtccata aggtctgaca acagcttgcc aaatttggtt agtccttgga tcagagcctg 2563

ttgtgggagg tagggaggaa atatgtaaag aaaaacagga agatacctgc actaatcatt 2623

cagacttcat tgagctctgc aaactttgcc tgtttgctat tggctacctt gatttgaaat 2683

gctttgtgaa aaaaggcact tttaacatca tagccacaga aatcaagtgc cagtctatct 2743

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 1               5                  10                  15

Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro Ala Ser
            20                  25                  30

Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr
        35                  40                  45

Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn
    50                  55                  60

Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile
65                  70                  75                  80

Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg
                85                  90                  95

Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln Gln Leu
            100                 105                 110

Ile Leu Lys Asp Pro Lys Gln Xaa Asn Ser Ser Phe Lys Arg Thr Gly
        115                 120                 125

Met Glu Ser Gln Pro Xaa Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe
    130                 135                 140

Val Arg Leu Ser Phe Ser Phe Ile Lys Asn Glu Ser Asn Tyr His Pro
145                 150                 155                 160

Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn
                165                 170                 175

Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln
            180                 185                 190

His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe
        195                 200                 205

Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro
    210                 215                 220

Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser
225                 230                 235                 240

Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val
                245                 250                 255

Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro
            260                 265                 270

Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val
        275                 280                 285

Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys
    290                 295                 300

Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser
305                 310                 315                 320
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Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg
                325                 330                 335

Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn
            340                 345                 350

His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys
        355                 360                 365

Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg
    370                 375                 380

Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe
385                 390                 395                 400

Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys
                405                 410                 415

Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu
            420                 425                 430

Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys
        435                 440                 445

Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp
    450                 455                 460

Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys
465                 470                 475                 480

Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser
                485                 490                 495

Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser
            500                 505                 510

Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala
        515                 520                 525

Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu
    530                 535                 540

Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro
545                 550                 555                 560

Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys
                565                 570                 575

Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val
            580                 585                 590

Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly
        595                 600                 605

Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala
    610                 615                 620

Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp
625                 630                 635                 640
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Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu
645 650 655

Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr
660 665 670

Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu
675 680 685

Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys
690 695 700

Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val Ala
705 710 715 720

Pro Leu

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tggnnnggng tnggnccngc nwsnmgnaay wsnggnytnt ayaayathac nttyaartay 180

gayaaytgya cnacntayyt naayccngtn ggnaarcayg tnathgcnga ygcncaraay 240

athacnathw sncartaygc ntgycaygay cargtngcng tnacnathyt ntggwsnccn 300

ggngcnytng gnathgartt yytnaarggn ttymgngtna thytngarga rytnaarwsn 360

garggnmgnc arnnncarca rytnathytn aargayccna arcarnnnaa ywsnwsntty 420

aarmgnacng gnatggarws ncarccnnnn ytnaayatga arttygarac ngaytaytty 480

gtnmgnytnw snttywsntt yathaaraay garwsnaayt aycayccntt yttyttymgn 540

acnmgngcnt gygayytnyt nytncarccn gayaayytng cntgyaarcc nttytggaar 600

ccnmgnaayy tnaayathws ncarcayggn wsngayatgc argtnwsntt ygaycaygcn 660

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ttyaarmgna aracntgyaa rcargarcar acnacngara tgacnwsntg yytnytncar 780

aaygtnwsnc cnggngayta yathathgar ytngtngayg ayacnaayac nacnmgnaar 840

gtnatgcayt aygcnytnaa rccngtncay wsnccntggg cnggnccnat hmgngcngtn 900

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acntayacng cngcnytncc nmgngarmgn ytnmgnccnm gnccnaargt nttyytntgy 1080
taywsnwsna argayggnca raaycayatg aaygtngtnc artgyttygc ntayttyytn 1140
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garggncarm gngartgggt nathcaraar athcaygarw sncarttyat hathgtngtn 1260
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tgyytnaarg tngargcngc ngtnytnggn gcnacnggnc cngcngayws ncarcaygar 1860
wsncarcayg gnggnytnga ycargayggn gargcnmgnc cngcnytnga yggnwsngcn 1920
gcnytncarc cnytnytnca yacngtnaar gcnggnwsnc cnwsngayat gccnmgngay 1980
wsnggnatht aygaywsnws ngtnccnwsn wsngarytnw snytnccnyt natggarggn 2040
ytnwsnacng aycaracnga racnwsnwsn ytnacngarw sngtnwsnws nwsnwsnggn 2100
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Homo sapiens

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gtc atc gac ctc tct gac tct gct ggg att ggc ttt cgc cac ctg ccc 96
Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro
-5 -1 1 5

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His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro
10 15 20 25

ata tcc ctt gcç gca cct ggt ggg ccc tct tct cca caa agc ctt ggt 192
Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly
30 35 40

gtg tgc gag tct ggc act gtt ccc gct gtt tgt gcc agc atc tgc tgt 240
Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys
45 50 55

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Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg
60 65 70

aat cca aaa agt ctt cca cat tca agt tct ata gga gac aca aga tgc 336
Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys
75 80 85

cag cac ctg ctc aga gga agc tgc tgc ctc gtc gtc acc tgt ctg aga 384
Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg
90 95 100 105

aga gcc atc aca ttt cca tcc cct ccc cag aca tct ccc aca agg gac 432
Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp
110 115 120

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Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val
125 130 135

ttc cca gat tgg act cac aaa ggc atg gag gtg ggc act ggg tac aac 528
Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn
140 145 150

agg aga tgg gtt cag ctg agt ggt gga ccc gag ttc tcc ttt gat ttg 576
Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu
155 160 165

ctg cct gag gcc cgg gct att cgg gtg acc ata tct tca ggc cct gag 624
Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu
170 175 180 185

gtc agc gtg cgt ctt tgt cac cag tgg gca ctg gag tgt gaa gag ctg 672
Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu
190 195 200

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agc agt ccc tat gat gtc cag aaa att gtg tct ggg ggc cac act gta    720
Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val
            205                 210                 215

gag ctg cct tat gaa ttc ctt ctg ccc tgt ctg tgc ata gag gca tcc    768
Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser
        220                 225                 230

tac ctg caa gag gac act gtg agg cgc aaa aaa tgt ccc ttc cag agc    816
Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser
    235                 240                 245

tgg cca gaa gcc tat ggc tcg gac ttc tgg aag tca gtg cac ttc act    864
Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr
250                 255                 260                 265

gac tac agc cag cac act cag atg gtc atg gcc ctg aca ctc cgc tgc    912
Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys
                270                 275                 280

cca ctg aag ctg gaa gct gcc ctc tgc cag agg cac gac tgg cat acc    960
Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr
            285                 290                 295

ctt tgc aaa gac ctc ccg aat gcc acg gct cga gag tca gat ggg tgg    1008
Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp
        300                 305                 310

tat gtt ttg gag aag gtg gac ctg cac ccc cag ctc tgc ttc aag gta    1056
Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val
    315                 320                 325

caa cca tgg ttc tct ttt gga aac agc agc cat gtt gaa tgc ccc cac    1104
Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His
330                 335                 340                 345

cag act ggg tct ctc aca tcc tgg aat gta agc atg gat acc caa gcc    1152
Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala
                350                 355                 360

cag cag ctg att ctt cac ttc tcc tca aga atg cat gcc acc ttc agt    1200
Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser
            365                 370                 375

gct gcc tgg agc ctc cca ggc ttg ggg cag gac act ttg gtg ccc ccc    1248
Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro
        380                 385                 390

gtg tac act gtc agc cag gtg tgg cgg tca gat gtc cag ttt gcc tgg    1296
Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp
    395                 400                 405

aag cac ctc ttg tgt cca gat gtc tct tac aga cac ctg ggg ctc ttg    1344
Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu
410                 415                 420                 425

atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg gcc    1392
Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala
                430                 435                 440
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Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val
445 450 455

ctc ctc ctg cac gcg gcg gac tcg gag gcg cag cgg cgc ctg gtg gga 1488
Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly
460 465 470

gcg ctg gct gaa ctg cta cgg gca gcg ctg ggc ggc ggg cgc gac gtg 1536
Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val
475 480 485

atc gtg gac ctg tgg gag ggg agg cac gtg gcg cgc gtg ggc ccg ctg 1584
Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu
490 495 500 505

ccg tgg ctc tgg gcg gcg cgg acg cgc gta gcg cgg gag cag ggc act 1632
Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr
510 515 520

gtg ctg ctg ctg tgg agc ggc gcc gac ctt cgc ccg gtc agc ggc ccc 1680
Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro
525 530 535

gac ccc cgc gcc gcg ccc ctg ctc gcc ctg ctc cac gct gcc ccg cgc 1728
Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg
540 545 550

ccg ctg ctg ctg ctc gct tac ttc agt cgc ctc tgc gcc aag ggc gac 1776
Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp
555 560 565

atc ccc ccg ccg ctg cgc gcc ctg ccg cgc tac cgc ctg ctg cgc gac 1824
Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp
570 575 580 585

ctg ccg cgt ctg ctg cgg gcg ctg gac gcg cgg cct ttc gca gag gcc 1872
Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala
590 595 600

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Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu
605 610 615

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Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu
620 625 630

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Gly

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His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro
10                  15                  20                  25

Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly
                30                  35                  40

Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys
            45                  50                  55

Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg
        60                  65                  70

Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys
    75                  80                  85

Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg
90                  95                  100                 105

Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp
                110                 115                 120

Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val
            125                 130                 135

Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn
        140                 145                 150

Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu
    155                 160                 165

Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu
170                 175                 180                 185

Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu
                190                 195                 200

Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val
            205                 210                 215

Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser
        220                 225                 230

Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser
    235                 240                 245

Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr
250                 255                 260                 265

Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys
                270                 275                 280

Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr
            285                 290                 295

Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp
        300                 305                 310
```

Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val
315 320 325

Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His
330 335 340 345

Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala
350 355 360

Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser
365 370 375

Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro
380 385 390

Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp
395 400 405

Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu
410 415 420 425

Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala
430 435 440

Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val
445 450 455

Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly
460 465 470

Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val
475 480 485

Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu
490 495 500 505

Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr
510 515 520

Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro
525 530 535

Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg
540 545 550

Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp
555 560 565

Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp
570 575 580 585

Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala
590 595 600

Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu
605 610 615

Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu
620 625 630

Gly

<210> 18
<211> 1971
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(1971)
<223> n may be a, c, g, or t

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wsngaywsng cnggnathgg nttymgncay ytnccncayt ggaayacnmg ntgyccnytn 120

gcnwsncaya cngargtnyt nccnathwsn ytngcngcnc cnggnggncc nwsnwsnccn 180

carwsnytng gngtntgyga rwsnggnacn gtnccngcng tntgygcnws nathtgytgy 240

cargtngcnc argtnttyaa yggngcnwsn wsnacnwsnt ggtgymgnaa yccnaarwsn 300

ytnccncayw snwsnwsnat hggngayacn mgntgycarc ayytnytnmg nggnwsntgy 360

tgyytngtng tnacntgyyt nmgnmgngcn athacnttyc cnwsnccncc ncaracnwsn 420

ccnacnmgng ayttygcnyt naarggnccn aayytnmgna thcarmgnca yggnaargtn 480

ttyccngayt ggacncayaa rggnatggar gtnggnacng gntayaaymg nmgntgggtn 540

carytnwsng gnggnccnga rttywsntty gayytnytnc cngargcnmg ngcnathmgn 600

gtnacnathw snwsnggncc ngargtnwsn gtnmgnytnt gycaycartg ggcnytngar 660

tgygargary tnwsnwsncc ntaygaygtn caraarathg tnwsnggngg ncayacngtn 720

garytnccnt aygarttyyt nytnccntgy ytntgyathg argcnwsnta yytncargar 780

gayacngtnm gnmgnaaraa rtgyccntty carwsntggc cngargcnta yggnwsngay 840

ttytggaarw sngtncaytt yacngaytay wsncarcaya cncaratggt natggcnytn 900

acnytnmgnt gyccnytnaa rytngargcn gcnytntgyc armgncayga ytggcayacn 960

ytntgyaarg ayytnccnaa ygcnacngcn mgngarwsng ayggntggta ygtnytngar 1020

aargtngayy tncayccnca rytntgytty aargtncarc cntggttyws nttyggnaay 1080

wsnwsncayg tngartgycc ncaycaracn ggnwsnytna cnwsntggaa ygtnwsnatg 1140

gayacncarg cncarcaryt nathytncay ttywsnwsnm gnatgcaygc nacnttywsn 1200

gcngcntggw snytnccngg nytnggncar gayacnytng tnccnccngt ntayacngtn 1260

wsncargtnt ggmgnwsnga ygtncartty gcntggaarc ayytnytntg yccngaygtn 1320

wsntaymgnc ayytnggnyt nytnathytn gcnytnytng cnytnytnac nytnytnggn 1380

gtngtnytng cnytnacntg ymgnmgnccn carwsnggnc cnggnccngc nmgnccngtn 1440

ytnytnytnc aygcngcnga ywsngargcn carmgnmgny tngtnggngc nytngcngar 1500

ytnytnmgng cngcnytngg nggnggnmgn gaygtnathg tngayytntg ggarggnmgn 1560

caygtngcnm gngtnggncc nytnccntgg ytntgggcng cnmgnacnmg ngtngcnmgn 1620

garcarggna cngtnytnyt nytntggwsn ggngcngayy tnmgnccngt nwsnggnccn 1680

gayccnmgng cngcnccnyt nytngcnytn ytncaygcng cnccnmgncc nytnytnytn 1740

ytngcntayt tywsnmgnyt ntgygcnaar ggngayathc cnccnccnyt nmgngcnytn 1800

ccnmgntaym gnytnytnmg ngayytnccn mgnytnytnm gngcnytnga ygcnmgnccn 1860

ttygcngarg cnacnwsntg gggnmgnytn ggngcnmgnc armgnmgnca rwsnmgnytn 1920

garytntgyw snmgnytnga rmgngargcn gcnmgnytng cngayytngg n 1971

<210> 19
<211> 808
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:rodent; surmised
Mus musculus

<220>
<221> CDS
<222> (78)..(806)

<220>
<221> mat_peptide
<222> (147)..(806)

<400> 19
cagctccggg ccaggccctg ctgccctctt gcagacagga aagacatggt ctctgcgccc 60

tgatcctaca gaagctc atg ggg agc ccc aga ctg gca gcc ttg ctc ctg 110
Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu
-20 -15

tct ctc ccg cta ctg ctc atc ggc ctc gct gtg tct gct cgg gtt gcc 158
Ser Leu Pro Leu Leu Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala
-10 -5 -1 1

tgc ccc tgc ctg cgg agt tgg acc agc cac tgt ctc ctg gcc tac cgt 206
Cys Pro Cys Leu Arg Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg
5 10 15 20

gtg gat aaa cgt ttt gct ggc ctt cag tgg ggc tgg ttc cct ctc ttg 254
Val Asp Lys Arg Phe Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu
25 30 35

gtg agg aaa tct aaa agt cct cct aaa ttt gaa gac tat tgg agg cac 302

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Val Arg Lys Ser Lys Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His
            40                  45                  50

agg aca cca gca tcc ttc cag agg aag ctg cta ggc agc cct tcc ctg     350
Arg Thr Pro Ala Ser Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu
        55                  60                  65

tct gag gaa agc cat cga att tcc atc ccc tcc tca gcc atc tcc cac     398
Ser Glu Glu Ser His Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His
    70                  75                  80

aga ggc caa cgc acc aaa agg gcc cag cct tca gct gca gaa gga aga     446
Arg Gly Gln Arg Thr Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg
85                  90                  95                  100

gaa cat ctc cct gaa gca ggg tca caa aag tgt gga gga cct gaa ttc     494
Glu His Leu Pro Glu Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe
                105                 110                 115

tcc ttt gat ttg ctg ccc gag gtg cag gct gtt cgg gtg act att cct     542
Ser Phe Asp Leu Leu Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro
            120                 125                 130

gca ggc ccc aag gca cgt gtg cgc ctt tgt tat cag tgg gca ctg gaa     590
Ala Gly Pro Lys Ala Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu
        135                 140                 145

tgt gaa gac ttg agt agc cct ttt gat acc cag aaa att gtg tct gga     638
Cys Glu Asp Leu Ser Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly
    150                 155                 160

ggg cac act gta gac ctg cct tat gaa ttc ctt ctg ccc tgc atg tgc     686
Gly His Thr Val Asp Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys
165                 170                 175                 180

ata gag gcc tcc tac ctg caa gag gac act gtg agg cgc aaa agt gtc     734
Ile Glu Ala Ser Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val
                185                 190                 195

cct tcc aga gct ggc ctg aag ctt atg gct cag act tct ggc agt caa     782
Pro Ser Arg Ala Gly Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln
            200                 205                 210

tac gct tca ctg act aca gcc agc ac                                  808
Tyr Ala Ser Leu Thr Thr Ala Ser
        215                 220
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<210> 20
<211> 243
<212> PRT
<213> Unknown

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<400> 20
Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu
            -20                 -15                 -10

Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
        -5                  -1  1               5
```

Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
10 15 20 25

Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
30 35 40

Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
45 50 55

Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
60 65 70

Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
75 80 85

Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
90 95 100 105

Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
110 115 120

Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
125 130 135

Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
140 145 150

Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
155 160 165

Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
170 175 180 185

Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val Pro Ser Arg Ala Gly
190 195 200

Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln Tyr Ala Ser Leu Thr
205 210 215

Thr Ala Ser
220

<210> 21
<211> 729
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(729)
<223> n may be a, c, g, or t

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gcngtnwsng cnmgngtngc ntgyccntgy ytnmgnwsnt ggacnwsnca ytgyytnytn 120

gcntaymgng tngayaarmg nttygcnggn ytncartggg gntggttycc nytnytngtn 180

mgnaarwsna arwsnccncc naarttygar gaytaytggm gncaymgnac nccngcnwsn 240

ttycarmgna arytnytngg nwsnccnwsn ytnwsngarg arwsncaymg nathwsnath 300

ccnwsnwsng cnathwsnca ymgnggncar mgnacnaarm gngcncarcc nwsngcngcn 360

garggnmgng arcayytncc ngargcnggn wsncaraart gyggnggncc ngarttywsn 420

ttygayytny tnccngargt ncargcngtn mgngtnacna thccngcngg nccnaargcn 480

mgngtnmgny tntgytayca rtgggcnytn gartgygarg ayytnwsnws nccnttygay 540

acncaraara thgtnwsngg nggncayacn gtngayytnc cntaygartt yytnytnccn 600

tgyatgtgya thgargcnws ntayytncar gargayacng tnmgnmgnaa rwsngtnccn 660

wsnmgngcng gnytnaaryt natggcncar acnwsnggnw sncartaygc nwsnytnacn 720

acngcnwsn 729

<210> 22
<211> 2377
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>
<221> CDS
<222> (180)..(1874)

<400> 22
ttttgagcag aggcttccta ggctccgtag aaatttgcat acagcttcca cttcctgctt 60

cagagcctgt tcttctactt acctgggccc ggagaaggtg gagggagacg agaagccgcc 120

gagagccgac taccctccgg gcccagtctg tctgtccgtg gtggatctaa gaaactaga 179

```
atg aac cga agc att cct gtg gag gtt gat gaa tca gaa cca tac cca     227
Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
  1               5                  10                  15

agt cag ttg ctg aaa cca atc cca gaa tat tcc ccg gaa gag gaa tca     275
Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
             20                  25                  30

gaa cca cct gct cca aat ata agg aac atg gca ccc aac agc ttg tct     323
Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
         35                  40                  45

gca ccc aca atg ctt cac aat tcc tcc gga gac ttt tct caa gct cac     371
Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
     50                  55                  60

tca acc ctg aaa ctt gca aat cac cag cgg cct gta tcc cgg cag gtc     419
Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
 65                  70                  75                  80
```

```
acc tgc ctg cgc act caa gtt ctg gag gac agt gaa gac agt ttc tgc   467
Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys
                85                  90                  95

agg aga cac cca ggc ctg ggc aaa gct ttc cct tct ggg tgc tct gca   515
Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala
            100                 105                 110

gtc agc gag cct gcg tct gag tct gtg gtt gga gcc ctc cct gca gag   563
Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu
        115                 120                 125

cat cag ttt tca ttt atg gaa aaa cgt aat caa tgg ctg gta tct cag   611
His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln
    130                 135                 140

ctt tca gcg gct tct cct gac act ggc cat gac tca gac aaa tca gac   659
Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp
145                 150                 155                 160

caa agt tta cct aat gcc tca gca gac tcc ttg ggc ggt agc cag gag   707
Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu
                165                 170                 175

atg gtg caa cgg ccc cag cct cac agg aac cga gca ggc ctg gat ctg   755
Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu
            180                 185                 190

cca acc ata gac acg gga tat gat tcc cag ccc cag gat gtc ctg ggc   803
Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly
        195                 200                 205

atc agg cag ctg gaa agg ccc ctg ccc ctc acc tcc gtg tgt tac ccc   851
Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro
    210                 215                 220

cag gac ctc ccc aga cct ctc agg tcc agg gag ttc cct cag ttt gaa   899
Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu
225                 230                 235                 240

cct cag agg tat cca gca tgt gca cag atg ctg cct ccc aat ctt tcc   947
Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser
                245                 250                 255

cca cat gct cca tgg aac tat cat tac cat tgt cct gga agt ccc gat   995
Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp
            260                 265                 270

cac cag gtg cca tat ggc cat gac tac cct cga gca gcc tac cag caa   1043
His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln
        275                 280                 285

gtg atc cag ccg gct ctg cct ggg cag ccc ctg cct gga gcc agt gtg   1091
Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val
    290                 295                 300

aga ggc ctg cac cct gtg cag aag gtt atc ctg aat tat ccc agc ccc   1139
Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro
305                 310                 315                 320
```

tgg gac caa gaa gag agg ccc gca cag aga gac tgc tcc ttt ccg ggg 1187
Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly
325 330 335

ctt cca agg cac cag gac cag cca cat cac cag cca cct aat aga gct 1235
Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala
340 345 350

ggt gct cct ggg gag tcc ttg gag tgc cct gca gag ctg aga cca cag 1283
Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln
355 360 365

gtt ccc cag cct ccg tcc cca gct gct gtg cct aga ccc cct agc aac 1331
Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn
370 375 380

cct cca gcc aga gga act cta aaa aca agc aat ttg cca gaa gaa ttg 1379
Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu
385 390 395 400

cgg aaa gtc ttt atc act tat tcg atg gac aca gct atg gag gtg gtg 1427
Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val
405 410 415

aaa ttc gtg aac ttt ttg ttg gta aat ggc ttc caa act gca att gac 1475
Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp
420 425 430

ata ttt gag gat aga atc cga ggc att gat atc att aaa tgg atg gag 1523
Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu
435 440 445

cgc tac ctt agg gat aag acc gtg atg ata atc gta gca atc agc ccc 1571
Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro
450 455 460

aaa tac aaa cag gac gtg gaa ggc gct gag tcg cag ctg gac gag gat 1619
Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp
465 470 475 480

gag cat ggc tta cat act aag tac att cat cga atg atg cag att gag 1667
Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu
485 490 495

ttc ata aaa caa gga agc atg aat ttc aga ttc atc cct gtg ctc ttc 1715
Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
500 505 510

cca aat gct aag aag gag cat gtg ccc acc tgg ctt cag aac act cat 1763
Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
515 520 525

gtc tac agc tgg ccc aag aat aaa aaa aac atc ctg ctg cgg ctg ctg 1811
Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
530 535 540

aga gag gaa gag tat gtg gct cct cca cgg ggg cct ctg ccc acc ctt 1859
Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu
545 550 555 560

cag gtg gtt ccc ttg tgacaccgtt catccccaga tcactgaggc caggccatgt 1914
Gln Val Val Pro Leu
565

ttggggcctt gttctgacag cattctggct gaggctggtc ggtagcactc ctggctggtt 1974

tttttctgtt cctccccgag aggccctctg gcccccagga aacctgttgt gcagagctct 2034

tccccggaga cctccacaca ccctggcttt gaagtggagt ctgtgactgc tctgcattct 2094

ctgcttttaa aaaaaccatt gcaggtgcca gtgtcccata tgttcctcct gacagtttga 2154

tgtgtccatt ctgggcctct cagtgcttag caagtagata atgtaaggga tgtggcagca 2214

aatggaaatg actacaaaca ctctcctatc aatcacttca ggctactttt atgagttagc 2274

cagatgcttg tgtatcctca gaccaaactg attcatgtac aaataataaa atgtttactc 2334

ttttgtaaaa aaaaaaaaaa aaaaaaaaag aaaaaaaaaa aaa 2377

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<212> PRT
<213> Unknown

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Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
1 5 10 15

Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
20 25 30

Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
35 40 45

Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
50 55 60

Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
65 70 75 80

Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys
85 90 95

Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala
100 105 110

Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu
115 120 125

His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln
130 135 140

Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp
145 150 155 160

Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu
165 170 175

```
Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu
            180                 185                 190

Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly
        195                 200                 205

Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro
    210                 215                 220

Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu
225                 230                 235                 240

Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser
                245                 250                 255

Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp
            260                 265                 270

His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln
        275                 280                 285

Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val
    290                 295                 300

Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro
305                 310                 315                 320

Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly
                325                 330                 335

Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala
            340                 345                 350

Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln
        355                 360                 365

Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn
    370                 375                 380

Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu
385                 390                 395                 400

Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val
                405                 410                 415

Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp
            420                 425                 430

Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu
        435                 440                 445

Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro
    450                 455                 460

Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp
465                 470                 475                 480

Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu
                485                 490                 495
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Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
500 505 510

Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
515 520 525

Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
530 535 540

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gtntgytayc cncargayyt nccnmgnccn ytnmgnwsnm gngarttycc ncarttygar 720

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ggngcnwsng tnmgnggnyt ncayccngtn caraargtna thytnaayta yccnwsnccn 960

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mgnaargtnt tyathacnta ywsnatggay acngcnatgg argtngtnaa rttygtnaay 1260

ttyytnytng tnaayggntt ycaracngcn athgayatht tygargaymg nathmgnggn 1320

athgayatha thaartggat ggarmgntay ytnmgngaya aracngtnat gathathgtn 1380

gcnathwsnc cnaartayaa rcargaygtn garggngcng arwsncaryt ngaygargay 1440

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ggnwsnatga ayttymgntt yathccngtn ytnttyccna aygcnaaraa rgarcaygtn 1560

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Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro
20 25 30

tcc cca cag gcc cca tgg aac tgt cag tac tac tgc ccc gga ggg ccc 144
Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro
35 40 45

tac cac cac cag gtg cca cac ggc cat ggc tac cct cca gca gca gcc 192
Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
50 55 60

tac cag caa gta ctc cag cct gct ctg cct ggg cag gtc ctt cct ggg 240
Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
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tcc agc ccc caa gac caa gaa gag aga cct gca cag aga gac ttc tct    336
Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser
            100                 105                 110

ttc ccg agg ctc ccg agg gac cag ctc tac cgc cca cca tct aat gga    384
Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly
        115                 120                 125

gtg gaa gcc cct gag gag tcc ttg gac ctt cct gca gag ctg aga cca    432
Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro
    130                 135                 140

cat ggt ccc cag gct cca tcc cta gct gcc gtg cct aga ccc cct agc    480
His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser
145                 150                 155                 160

aac ccc tta gcc cga gga act cta aga acc agc aat ttg cca gaa gaa    528
Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu
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tta cgg aaa gtc ttt atc act tat tct atg gac aca gcc atg gag gtg    576
Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val
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Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile
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gac ata ttt gag gat aga atc cgg ggt att gat atc att aaa tgg atg    672
Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met
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gag cgc tat ctt cga gat aag aca gtg atg ata atc gta gca atc agc    720
Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser
225                 230                 235                 240

ccc aaa tac aaa cag gat gtg gaa ggc gct gag tcg cag ctg gac gag    768
Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu
                245                 250                 255

gac gag cat ggc tta cat act aag tac att cat cgg atg atg cag att    816
Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile
            260                 265                 270

gag ttc ata agt cag gga agc atg aac ttc aga ttc atc cct gtg ctc    864
Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu
        275                 280                 285

ttc cca aat gcc aag aag gag cat gtg ccg acc tgg ctt cag aac act    912
Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr
    290                 295                 300

cat gtt tac agc tgg ccc aag aat aag aaa aac atc ctg ctg cgg ctg    960
His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu
305                 310                 315                 320
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ctt cag gtg gta ccc ttg tgacgatggc cactccagct cagtgccagc 1056
Leu Gln Val Val Pro Leu
340

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cttctacaga gtcctctgtc tcctgagtct gagttgtcct cgctgggctt ccagagcttc 1176

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35 40 45

Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
50 55 60

Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
65 70 75 80

Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp
85 90 95

Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser
100 105 110

Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly
115 120 125

Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro
130 135 140

His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser
145 150 155 160

Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu
165 170 175

Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val

180 185 190

Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile
195 200 205

Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met
210 215 220

Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser
225 230 235 240

Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu
245 250 255

Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile
260 265 270

Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu
275 280 285

Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr
290 295 300

His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu
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Leu Gln Val Val Pro Leu
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cartaytayt gyccnggngg nccntaycay caycargtnc cncayggnca yggntayccn 180

ccngcngcng cntaycarca rgtnytncar ccngcnytnc cnggncargt nytnccnggn 240

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garytnmgnc cncayggncc ncargcnccn wsnytngcng cngtnccnmg nccnccnwsn 480

aayccnytng cnmgnggnac nytnmgnacn wsnaayytnc cngargaryt nmgnaargtn 540

ttyathacnt aywsnatgga yacngcnatg gargtngtna arttygtnaa yttyytnytn 600

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ccnaartaya arcargaygt ngarggngcn garwsncary tngaygarga ygarcayggn 780

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aayttymgnt tyathccngt nytnttyccn aaygcnaara argarcaygt nccnacntgg 900

ytncaraaya cncaygtnta ywsntggccn aaraayaara araayathyt nytnmgnytn 960

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35 40 45

Met Thr Trp Val Gly Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser
50 55 60

Lys Ile Ile Val Leu Cys Ser Arg Gly Thr Arg Ala Lys Trp Gln Ala
65 70 75 80

Leu Leu Gly Arg Gly Ala Pro Val Arg Leu Arg Cys Asp His Gly Lys
85 90 95

Pro Val Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro Asp
100 105 110

Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe Ser
115 120 125

Glu Val Ser Cys Asp Gly Asp Val Pro Asp Leu Phe Gly Ala Ala Pro
130 135 140

Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile Gln
145 150 155 160

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Asp Leu Glu Met Phe Gln Pro Gly Arg Met His Arg Val Gly Glu Leu
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Ser Gly Asp Asn Tyr Leu Arg Ser Pro Gly Gly Arg Gln Leu Arg Ala
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     50                  55                  60

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 65                  70                  75                  80

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                 85                  90                  95

Lys Pro Ala Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro
            100                 105                 110

Asp Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe
        115                 120                 125

Ser Gly Ile Cys Ser Glu Arg Asp Val Pro Asp Leu Phe Asn Ile Thr
    130                 135                 140

Ser Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile
145                 150                 155                 160

Gln Asp Leu Glu Met Phe Glu Pro Gly Arg Met His His Val Arg Glu
                165                 170                 175

Leu Thr Gly Asp Asn Tyr Leu Gln Ser Pro Ser Gly Arg Gln Leu Lys
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Glu Ala Val Leu Arg Phe Gln Glu Trp Gln Thr Gln Cys Pro Asp Trp
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Pro Val Phe Asp Leu Glu Lys Leu Ile Thr Ala Glu Ile Val Pro Ser
         35                  40                  45

Arg Trp Leu Val Asp Gln Ile Ser Ser Leu Lys Lys Phe Ile Ile Val
     50                  55                  60

Val Ser Asp Cys Ala Glu Lys Ile Leu Asp Thr Glu Ala Ser Glu Thr
 65                  70                  75                      80

His Gln Leu Val Gln Ala Arg Pro Phe Ala Asp Leu Phe Gly Pro Ala
                 85                  90                  95

Met Glu Met Ile Ile Arg Asp Ala Thr His Asn Phe Pro Glu Ala Arg
            100                 105                 110

Lys Lys Tyr Ala Val Val Arg Phe Asn Tyr Ser Pro His Val Pro Pro
        115                 120                 125

Asn Leu Ala Ile Leu Asn Leu Pro Thr Phe Ile Pro Glu Gln Phe Ala
    130                 135                 140

Gln Leu Thr Ala Phe Leu His Asn Val Glu His Thr Glu Arg Ala Asn
145                 150                 155                     160

Val Thr Gln Asn Ile Ser Glu Ala Gln Ile His Glu Trp Asn Leu Cys
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35 40 45

Leu His Trp Val Tyr Glu Gln Thr Lys Ile Ala Glu Lys Ile Ile Val
50 55 60

Phe His Ser Ala Tyr Tyr His Pro Arg Cys Gly Ile Tyr Asp Val Ile
65 70 75 80

Asn Asn Phe Phe Pro Cys Thr Asp Pro Arg Leu Ala His Ile Ala Leu
85 90 95

Thr Pro Glu Ala Gln Arg Ser Val Pro Lys Glu Val Glu Tyr Val Leu
100 105 110

Pro Arg Asp Gln Lys Leu Leu Glu Asp Ala Phe Asp Ile Thr Ile Ala
115 120 125

Asp Pro Leu Val Ile Asp Ile Pro Ile Glu Asp Val Ala Ile Pro Glu
130 135 140

Asn Val Pro Ile His His Glu Ser Cys Asp Ser Ile Asp Ser Arg Asn
145 150 155 160

Asn Ser Lys Thr His Ser Thr Asp Ser Gly Val Ser Ser Leu Ser Ser
165 170 175

Asn Ser

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International Bureau

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(10) International Publication Number
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(74) Agent: ZARADIC, Sandy; Schering-Plough Corporation, Patent Department, K-6-1, 1990, 2000 Galloping Hill Road, Kenilworth, NJ 07033-0530 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, HR, HU, ID, IL, IN, IS, JP, KG, KR, KZ, LC, LK, LR, LT, LU, LV, MA, MD, MG, MK, MN, MX, MZ, NO, NZ, PL, PT, RO, RU, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UZ, VN, YU, ZA.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:
— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for all designations*

Published:
— *with international search report*

(88) Date of publication of the international search report: 23 January 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/090358 A3

(54) Title: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

(57) Abstract: Nucleic acids encoding mammalian, e.g., primate, receptors, purified receptor proteins and fragments thereof. Antibodies, both polyclonal and monoclonal, are also provided. Methods of using the compositions for both diagnostic and therapeutic utilities are described.

INTERNATIONAL SEARCH REPORT

Interr[redacted]al Application No
PCT/US 01/16767

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C07K14/715 C07K16/18 G01N33/53 C12N5/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

SEQUENCE SEARCH, EMBL, EPO-Internal, MEDLINE, BIOSIS, WPI Data, PAJ, CHEM ABS Data, SCISEARCH, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 96 29408 A (IMMUNEX CORP) 26 September 1996 (1996-09-26) page 2, line 35 -page 15, line 4 ---	1-18
X	YAO Z ET AL: "MOLECULAR CHARACTERIZATION OF THE HUMAN INTERLEUKIN (IL)-17 RECEPTOR" CYTOKINE, ACADEMIC PRESS LTD, PHILADELPHIA, PA, US, vol. 9, no. 11, November 1997 (1997-11), pages 794-800, XP000867704 ISSN: 1043-4666 page 795; figure 2 ---	1-4,6, 12-15

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"O" document referring to an oral disclosure, use, exhibition or other means

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"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
12 August 2002	29.08.02

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Steffen, P

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL 'Online! EBI; 18 February 2000 (2000-02-18) BLOECKER ET AL.: "Homo sapiens mRNA; cDNA DKFZp434N1928" Database accession no. AL133097 XP002183453 the whole document ---	1-4,6, 12-15
A	WO 99 14240 A (HUMAN GENOME SCIENCES INC ;RUBEN STEVEN M (US); SHI YANGGU (US)) 25 March 1999 (1999-03-25) the whole document ---	
A	TIAN E ET AL: "EVI27 ENCODES A NOVEL MEMBRANE PROTEIN WITH HOMOLOGY TO THE IL17 RECEPOR" ONCOGENE, BASINGSTOKE, HANTS, GB, vol. 19, no. 17, 20 April 2000 (2000-04-20), pages 2098-2109, XP008000240 ISSN: 0950-9232 the whole document ---	
A	SHI YANGGU ET AL: "A novel cytokine receptor-ligand pair: Identification, molecular characterization, and in vivo immunomodulatory activity." JOURNAL OF BIOLOGICAL CHEMISTRY (JBC PAPERS IN PRESS, DOI 10.1074/JBC.M910228199), vol. 275, no. 25, 3 April 2000 (2000-04-03), pages 19167-19176, XP002197927 ISSN: 0021-9258 the whole document ---	
A	FOSSIEZ F ET AL: "INTERLEUKIN-17" INTERNATIONAL REVIEWS OF IMMUNOLOGY, HARWOOD ACADEMIC PUBLISHERS, LONDON, GB, vol. 16, no. 5/6, 1998, pages 541-551, XP000867763 ISSN: 0883-0185 the whole document ---	
E	WO 01 68859 A (AMGEN INC ;JING SHUQIAN (US)) 20 September 2001 (2001-09-20) page 2, line 19 -page 10, line 27; examples 1-4 ---	1-18
E	WO 01 46420 A (GENENTECH INC) 28 June 2001 (2001-06-28) page 5, line 1 -page 16, line 17; figures 17,18 --- -/--	1-18

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 55865 A (GENESIS RES & DEV CORP LTD) 4 November 1999 (1999-11-04) SEQ ID NO's 125 and 303 and corresponding cDNA's page 3 -page 17	1-18
X	DATABASE EMBL 'Online! EBI; 22 July 1999 (1999-07-22) NCI-CGAP: "ty30c03.x1 NCI_CGAP_UT2 Homo sapiens cDNA clone IMAGE:2280580 3' mRNA sequence" Database accession no. AI861981 XP002209553 the whole document	12-18
X	DATABASE EMBL 'Online! EBI; 21 October 1999 (1999-10-21) MARRA ET AL.: "u191g04.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2159478 5', mRNA sequence" Database accession no. AW107583 XP002209554 the whole document	12-18

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/16767

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 19, 20
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-18 (all partly)

   Compositions comprising primate DCRS8 polypeptides and nucleic acid sequences (SEQ ID NO's 14 and 13, respectively) as well as further embodiments relating to the said polypeptides and nucleic acid sequences.

2. Claims: 1-18 (all partly)

   Compositions comprising primate or rodent DCRS9 polypeptides and nucleic acid sequences (SEQ ID NO's 16, 19 and 17, 20, respectively) as well as further embodiments relating to the said polypeptides and nucleic acid sequences.

FURTHER INF

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Claims

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International Application No
PCT/US 01/16767

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